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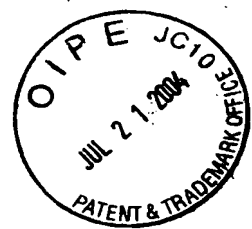
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1/60

5'                    9                    18                    27                    36                    45                    54  
GTG GGC ATG GTG GGC AAC GTC CTG CTG GTG CTG GTG ATC GCG CCG GTG CCG CCG  
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg

                  63                    72                    81                    90                    99                    108  
CTG CAC AAC GTG ACG AAC TTC CTC ATC GGC AAC CTG GCC TTG TCC GAC GTG CTC  
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu

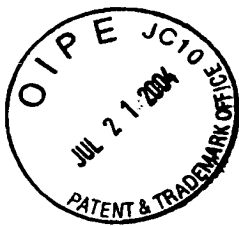
                  117                    126                    135                    144                    153                    162  
ATG TGC ACC GCC TGC GTG CCG CTC ACG CTG GCC TAT GCC TTC GAG CCA CGC GGC  
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly

                  171                    180                    189                    198                    207                    216  
TGG GTG TTC GGC GGC GGC CTG TGC CAC CTG GTC TTC TTC CTG CAG CCG GTC ACC  
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
Trp Val Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr

                  225                    234                    243                    252                    261                    270  
GTC TAT GTG TCG GTG TTC ACG CTC ACC ACC ATC GCA GTG GAC CCG TAC GTC GTG  
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr Val Val

                  279                    288                    297  
CTG GTG CAC CCG CTG AGG CCG CGC ATC 3'  
--- --- --- --- --- --- --- --- ---  
Leu Val His Pro Leu Arg Arg Arg Ile

FIG. 1



5'	9	18	27	36	45	54
CCC CTG CTG CTG ACC TAC CTG CTC CCT CTG CTG GTC ATC CTC CTG TCT TAC						
---						
Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr						
63	72	81	90	99	108	
GTC CGG GTG TCA GTG AAG CTC CGC AAC CGC GTG CTG CCG GGC TGC GTG ACC CAG						
---						
Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Cys Val Thr Gln						
117	126	135	144	153	162	
AGC CAG GCC GAC TGG GAC CGC GCT CGG CGC CGG CGC ACC TTC TGC TTG CTG GTG						
---						
Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val						
171	180	189	198			
GTG GTC GTG GTG TTT GCC ATC TGC TGC TTG CCT TAC TAC 3'						
---						
Val Val Val Val Val Phe Ala Ile Cys Trp Leu Pro Tyr Tyr						

FIG. 2

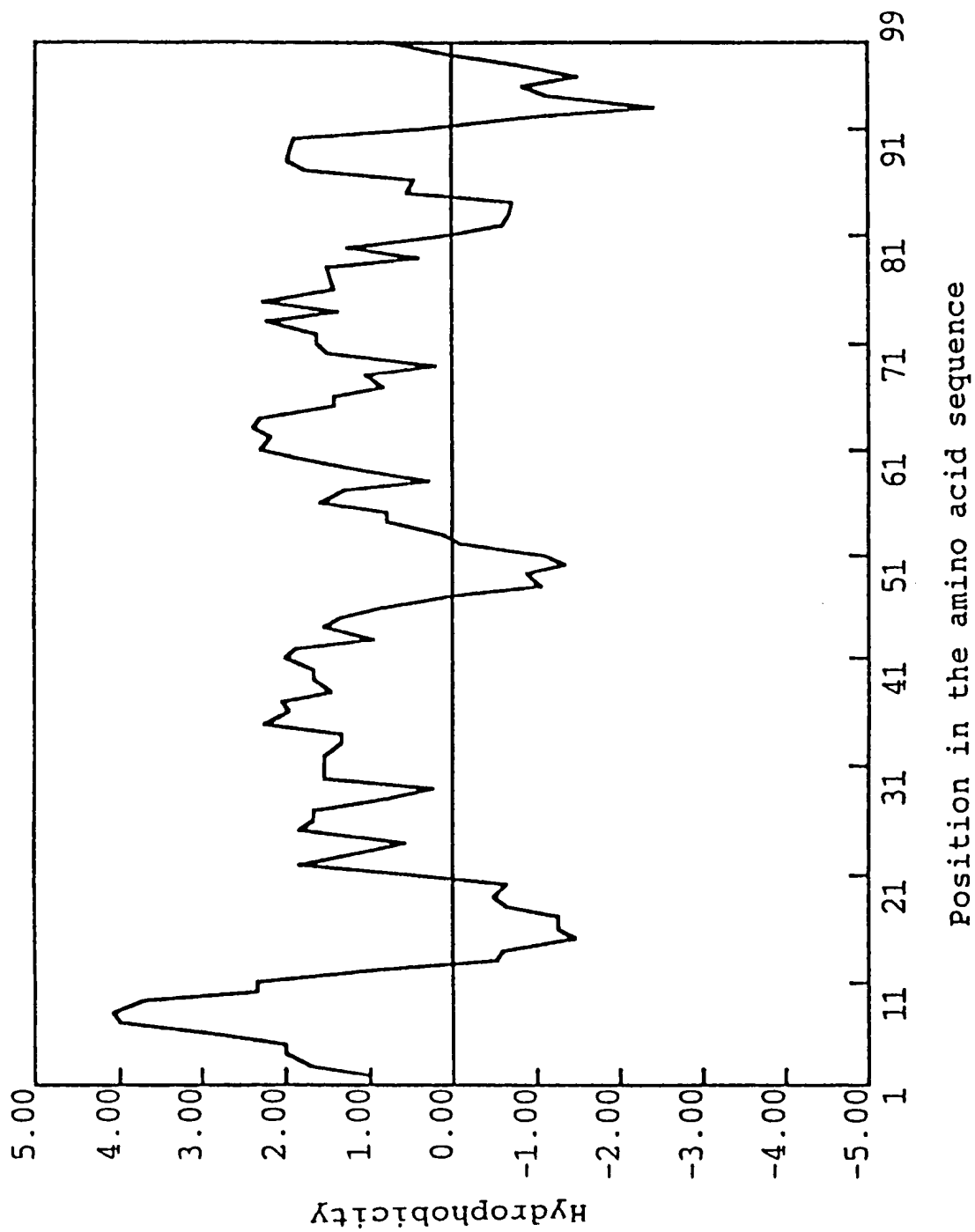


FIG. 3

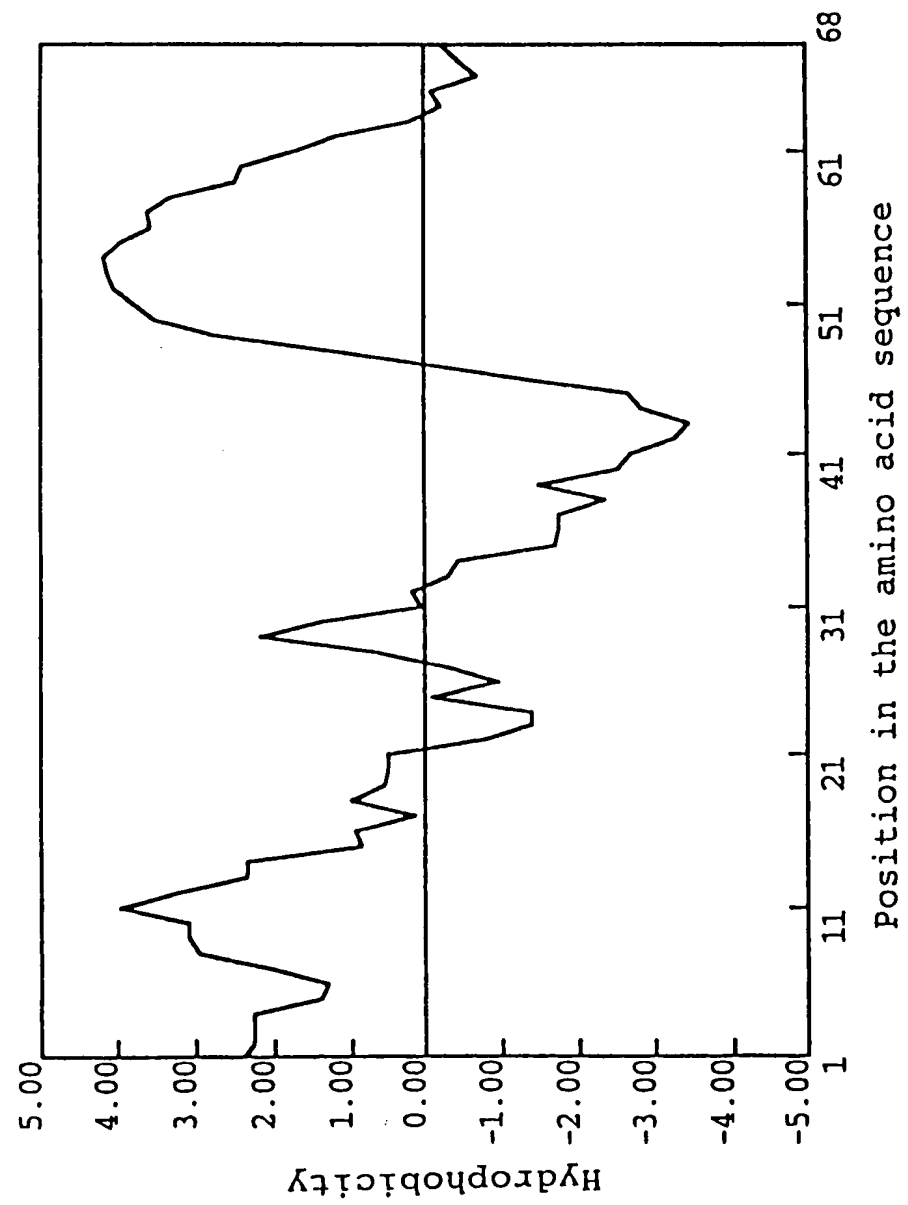
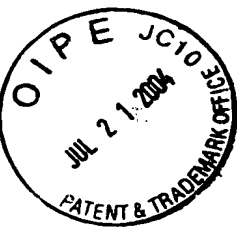


FIG. 4



FIG. 5

FIG. 6A
FIG. 6B
FIG. 6C

FIG. 6

6/60

5' 9 GTG GGC ATG GTG GGC AAC ATC CTG CTG CTG CTG 27 36 45 54  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Val Gly Met Val Val Gly Asn Ile Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg  
 63 72 81 90 99 108  
 CTG TAC AAC GTG ACG AAT TTC CTC ATC GGC AAC CTG GGC TTC TCC GAC GTG CTC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Leu Tyr Asn Val Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu  
 117 126 135 144 153 162  
 ATG TGC ACC GGC TGC GTG CCG CTC ACG CTG GGC TAT GGC TTC GAG CCA CGC GGC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly

FIG. 6A



FIG. 6B



441	450	459	468	477	486
TCC CAG GAG CGC CAG CGC CAG CTC TAC GCC TGG GGG CTG CTG GTC ACC TAC					
---	---	---	---	---	---
Ser Gln Glu Arg Gln Arg Gln Leu Tyr Ala Trp Gly Leu Leu Val Thr Tyr					
495	504	513	522	531	540
CTG CTC CCT CTG CTG ATC CTC CTG TCT TAC GCC CGG GTG TCA GTG AAG CTC					
---	---	---	---	---	---
Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu					
549	558	567	576	585	594
CGC AAC CGC GTG GTG CCG CGC CGC CGC ACC CAG AGC CAG GCC GAC TGG GAC CGC					
---	---	---	---	---	---
Arg Asn Arg Val Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg					
603	612	621	630	639	648
CCT CGC CGC CGC ACC TTC TGC TTC CTG CTG GTC GTG GTC TTC ACC					
---	---	---	---	---	---
Ala Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Phe Thr					
657	666				
CTC TGC TGG CTG CCC TTC TTC 3'					
---	---	---	---	---	---
Leu Cys Trp Leu Pro Phe Phe					

FIG. 6C

p19P2	1	10	20	30	40	50	
		1	2	3	4	5	
PG3-2/PG1-10	1	10	20	30	40	50	
		1	2	3	4	5	
p19P2	51	60	70	80	90	100	
		51	61	71	81	91	
PG3-2/PG1-10	51	60	70	80	90	100	
		51	61	71	81	91	
p19P2	101	110	120	130	140	150	
		101	111	121	131	141	
PG3-2/PG1-10	101	110	120	130	140	150	
		101	111	121	131	141	
p19P2	151	160	170	180	190	200	
		151	161	171	181	191	
PG3-2/PG1-10	151	160	170	180	190	200	
		151	161	171	181	191	
p19P2	201	210	220	230	240	250	
		201	211	221	231	241	
PG3-2/PG1-10	201	210	220	230	240	250	
		201	211	221	231	241	

FIG. 7

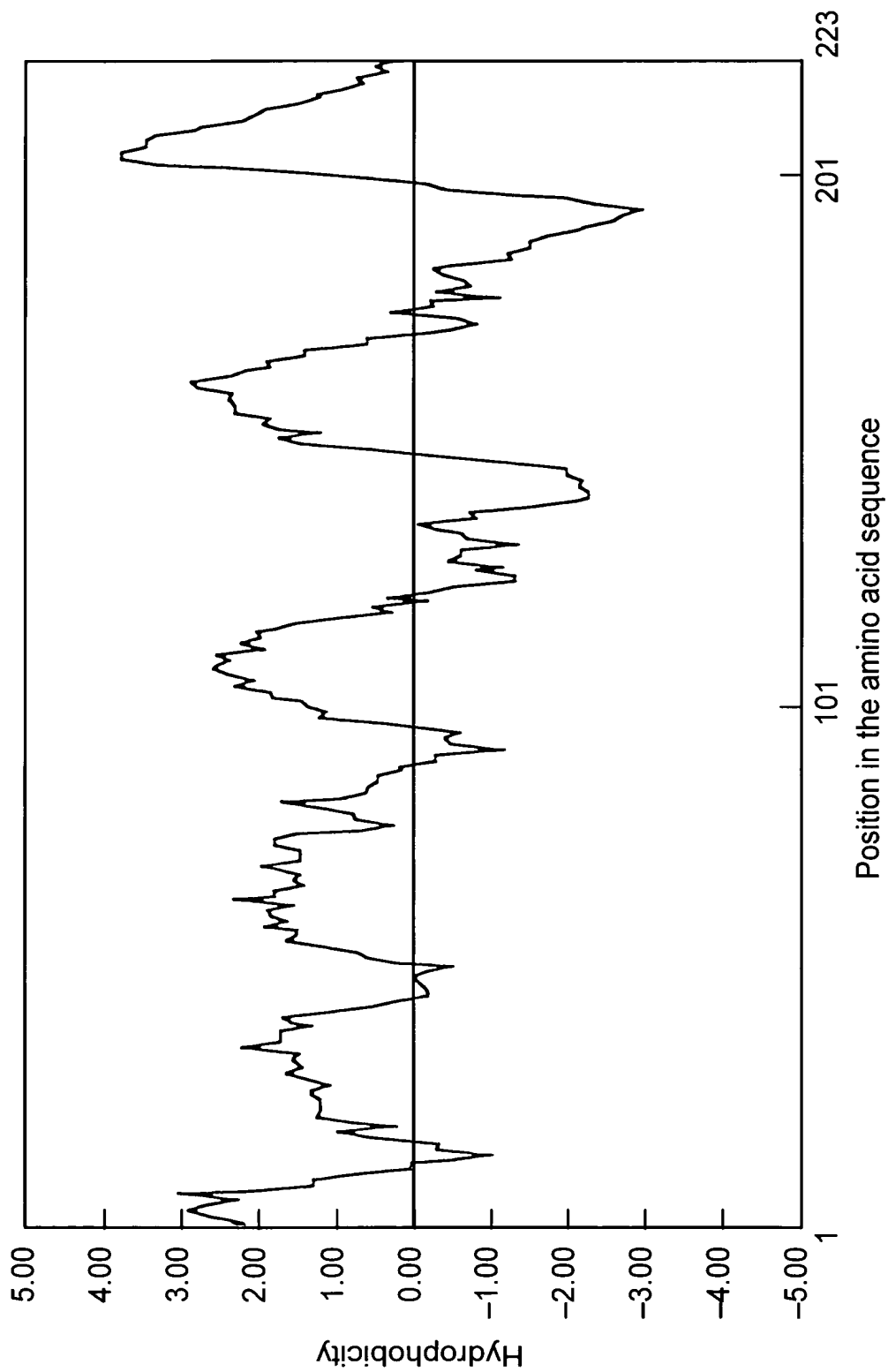


FIG. 8

FIG. 9A
FIG. 9B
FIG. 9C

FIG. 9

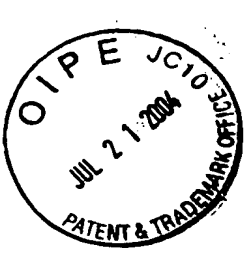
1 CATCGTCAAGCAGATGAAGATCATCCACGAGGATCGCTACTCCGAGGCCAGCAGAAATT 60  
 1  
 61 CTGCCCCCTTCTTCCCGCGAGTGCTTTCCCGCTCTCCAAACCCCACTCCAGGTGCCCATG 120  
 1 Met 1  
 121 GCCTCATCGACCACTCGGGGCCCCAGGGTTTCTGACTTATTTTCTGGGCTGCCCGCCGGCG 180  
 1 AlaSerSerThrThrArgGlyProArgValSerAspLeuPheSerGlyLeuProProAla 21  
 181 GTCACAACTCCCGCCAACCAAGCGCAGAGGCCCTCGCGCGCAACGGGTCTGGTGGCTGGC 240  
 21 ValThrThrProAlaAsnGlnSerAlaGluAlaSerAlaGlyAsnGlySerValAlaGly 41  
 241 GCGGACGCTCCAGCCGTACGCCCTTCCAGAGCCTGCAGCTGGTGCATCAGCTGAAGGG 300  
 41 AlaAspAlaProAlaValThrProPheGlnSerLeuGlnLeuValHisGlnLeuLysGly 61

11/60

FIG. 9A

301	CTGATCGTCTCTACAGCGTCTGTCGTCTGGGCTGTCGGCAACTGCCTGCTG	360
61	LeuIleValLeuLeuTyrSerValValValValGlyLeuValGlyAsnCysLeuLeu	81
361	GTGCTGGTATCGCGGGTGGCGGCTGCACAACGTGACGAACCTTCCTCATCGCAAC	420
81	ValLeuValIleAlaArgValArgArgLeuHisAsnValThrAsnPheLeuIleGlyAsn	101
421	CTGGCCTTGTCGACGTGCTCATGTGCACCGCCTGCGTGCCGCTCAGGCTGGCCTATGCC	480
101	LeuAlaLeuSerAspValLeuMetCysThrAlaCysValProLeuThrLeuAlaTyrAla	121
481	TTCGAGCCACGCGGCTGGGTGTCGGCGGCGCTGTGCCACCTGGTCTTCTTCCTGCAG	540
121	PheGluProArgGlyTrpValPheGlyGlyLeuCysHisLeuValPhePheLeuGln	141
541	CCGGTACCGTCTATGTGTCGGGTTCACGCTCACCATCCAGTCGACCGCTACGTC	600
141	ProValThrValTyrValSerValPheThrLeuThrThrIleAlaValAspArgTyrVal	161
601	GTGCTGGTCACCCGCTGAGCGCGGCATCTCGCTGCGCCTCAGCGCCTACGCTGTGCTG	660
161	ValLeuValHisProLeuArgArgIleSerLeuArgLeuSerAlaTyrAlaValLeu	181
661	GCCATCTGGCGCTGTCCGCGTGTGCGGCTGCCCGCGCGTGCACACCTATCACGTC	720
181	AlaIleTrpAlaLeuSerAlaValLeuAlaLeuProAlaAlaValHisThrTyrHisVal	201
721	GAGCTCAAGCCGACGACGTGCGCCTCTGCGAGGAGTTCTGGGGCTCCAGGAGCGCCAG	780
201	GluLeuLysProHisAspValArgLeuCysGluGluPheTrpGlySerGlnGluArgGln	221
781	CGCCAGCTCTACGCCCTGGGGGCTGCTGCTGCACCTACCTGCTCCCTCTGCTGTCATC	840
221	ArgGlnLeuTyrAlaTrpGlyLeuLeuLeuValThrTyrLeuLeuProLeuLeuValIle	241

FIG. 9B



13/60

841	CTCCTGTCTTACGTCGCGGTGTCAGTGAAGCTCCGCAACCGCGTGTGCCGGCTGCGTG	900
241	LeuLeuSerTyrValArgValSerValLysLeuArgAsnArgValValProGlyCysVal	261
901	ACCCAGAGCCAGCCGACTGGGACCGCGCTCGCGCCGCGCACCTTCTGCTTGTCTGGTG	960
261	ThrGlnSerGlnAlaAspTrpAspArgAlaArgArgArgThrPheCysLeuLeuVal	281
961	GTGGTCGTGGTGTTCGCCGCTCTGCTGGCTGCCGCTGCACGTCTTCAACCTGCTGCCG	1020
281	ValValValValPheAlaValCysTrpLeuProLeuHisValPheAsnLeuLeuArg	301
1021	GACCTCGACCCCAACGATCGACCCCTTACGCCCTTTGGCTGGTGCAGCTGCTTCCAC	1080
301	AspLeuAspProHisAlaIleAspProTyrAlaPheGlyLeuValGlnLeuLeuCysHis	321
1081	TGGCTCGCCATGAGTTTCGGCCTGCTACAACCCCTTCACTCTACGCCCTGGCTGCACGACGC	1140
321	TrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHisAspSer	341
1141	TTCCGCGAGGAGCTGCGCAACTGTTGGTGGCTGGCCCCCGCAAGATAGCCCCCATGGC	1200
341	PheArgGluGluLeuArgLysLeuLeuValAlaTrpProArgLysIleAlaProHisGly	361
1201	CAGAAATATGACCGTCAGCGTGGTCACTCTGATGCCACTTAGCCAGGCCCTTGGTCAAGGAGC	1260
361	GlnAsnMetThrValSerValValIle***	371
1261	TCCACTTCAACTGGCCTCCTAGCGCACCACTCGAGGTCAATCTGCTTATTCTCAGCA	1320
371		371
1321	CCAGAGCTAGC	1331
371		371

FIG. 9C

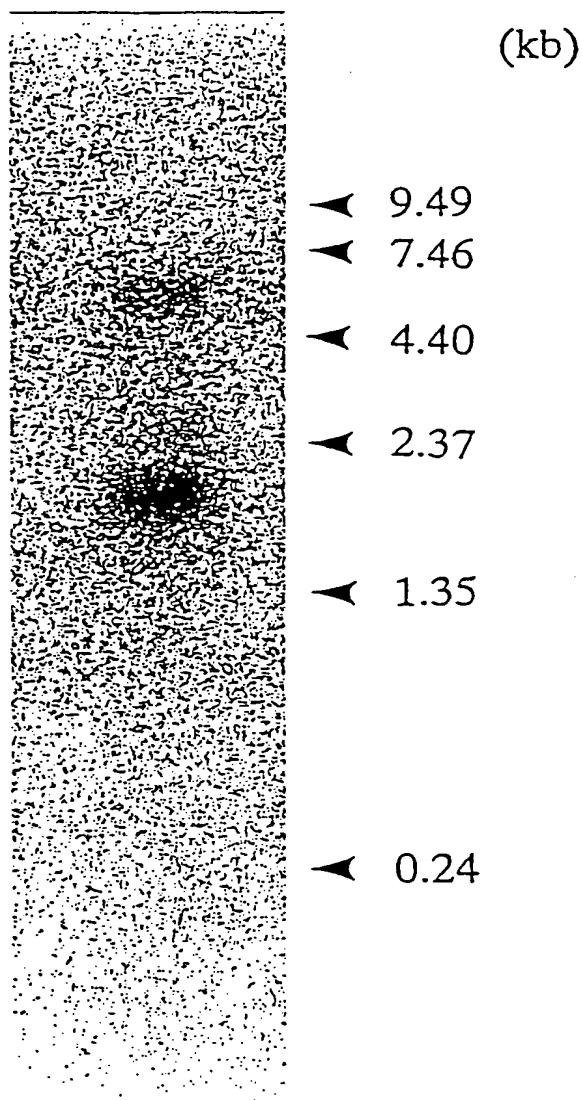


FIG. 10

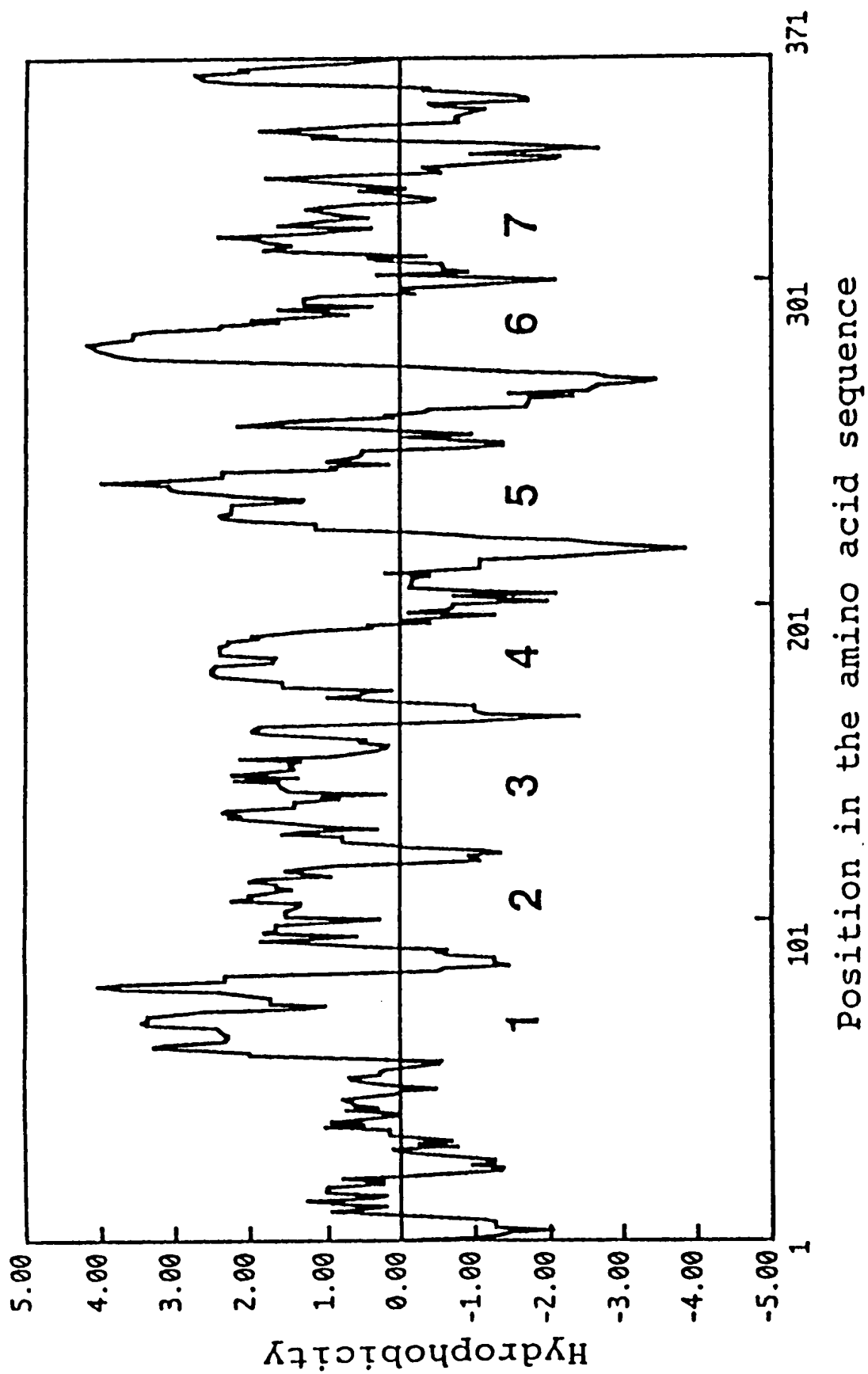
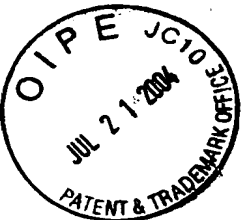


FIG. 11





16/60

5'                    9                    18                    27                    36                    45                    54  
 CTG TGT GTC ATC GCG GTG GAT AGG TAC GTG GTT CTG GTG CAC CCG CTA CGT CGG  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
Leu Cys Val Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg Arg

                  63                    72                    81                    90                    99                    108  
 CGC ATT TCA CTG AGG CTC AGC GCC TAC GCG GTG CTG GGC ATC TGG GCT CTA TCT  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser

                  117                    126                    135                    144                    153                    162  
 GCA GTG CTG GCG CTG CCG GCC GCG GTG CAC ACC TAC CAT GTG GAG CTC AAG CCC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Ala Val Leu Ala Leu Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro

                  171                    180                    189                    198                    207                    216  
 CAC GAC GTG AGC CTC TGC GAG GAG TTC TGG GGC TCG CAG GAG CCG CAA CGC CAG  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 His Asp Val Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln

                  225                    234                    243                    252                    261                    270  
 ATC TAC GCC TGG GGG CTG CTT CTG GGC ACC TAT TTG CTC CCC CTG CTG GCC ATC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Ile Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala Ile

                  279                    288                    297                    306                    315                    324  
 CTC CTG TCT TAC GTA CCG GTG TCA GTG AAG CTG AGG AAC CCG GTG GTG CCT GGC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly

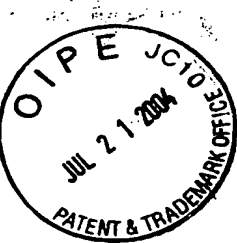
                  333                    342                    351                    360                    369                    378  
 AGC GTG ACC CAG AGT CAA GCT GAC TGG GAC CGA GCG CGT CCG CCG CCG ACT TTC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe

                  387                    396                    405                    414                    423                    432  
 TGT CTG CTG GTG GTG GTG GTG GTA GTG TTC ACG CTC TGC TGG CTG CCC TTC TAC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Cys Leu Leu Val Val Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Tyr

CT 3'

--  
 —

FIG. 12



p19P2	1	VGMVGNVLLV	10	LVIARVRRLLH	20	NVTNFLIGNL	30	ALSDVLMCTA	40	CVPLTLAYAF	50	50
pG3-2/pG1-10	1	VGMVGNVLLV		LVIARVRRLLY		NVTNFLIGNL		ALSDVLMCTA		CVPLTLAYAF		50
p5S38	-79	.....		.....		.....		.....		.....		-30
p19P2	51	EPRGMVFCGG	60	LCHLVFFLQp	70	VTVVVSVFTL	80	TTIAVDRYVV	90	LVHPLRRRI-	100	100
pG3-2/pG1-10	51	EPRGMVFCGG		LCHLVFFLQA		VTVVVSVFTL		TTIAVDRYVV		LVHPLRRRIIS		100
p5S38	-29	.....		.....		.....		CVIAVDRYVV		LVHPLRRRIIS		21
p19P2	101	-----	110	-----	120	-----	130	-----	140	-----	150	150
pG3-2/pG1-10	101	LRLSAYAVLA		IWL SAVLAL		PAAVHTYHVE		LKPHDVR LCE		EFWGSQERQR		150
p5S38	22	LRLSAYAVLG		IWA SAVLAL		PAAVHTYHVE		LKPHDVS LCE		EFWGSQERQR		71
p19P2	151	-----GLLLV	160	TYLLPLLVIL	170	LSYVRVSVKL	180	RNRVVPGCVT	190	QSQADWDRAR	200	200
pG3-2/pG1-10	151	QLYAMGLLV		TYLLPLLVIL		LSYA RVSVKL		RNRVVPGRVVT		QSQADWDRAR		200
p5S38	72	QIYAMGLLLG		TYLLPLLLAIL		LSYVRVSVKL		RNRVVPGSVT		QSQADWDRAR		121
p19P2	201	RRRTFCLLVV	210	VVVVFAICML	220	PFY.....	230	-----	240	-----	250	250
pG3-2/pG1-10	201	RRRTFCLLVV		VVVVFTLCML		PFF.....		-----		-----		250
p5S38	122	RRRTFCLLVV		VVVVFTLCML		PFY.....		-----		-----		171

FIG. 13

18/60

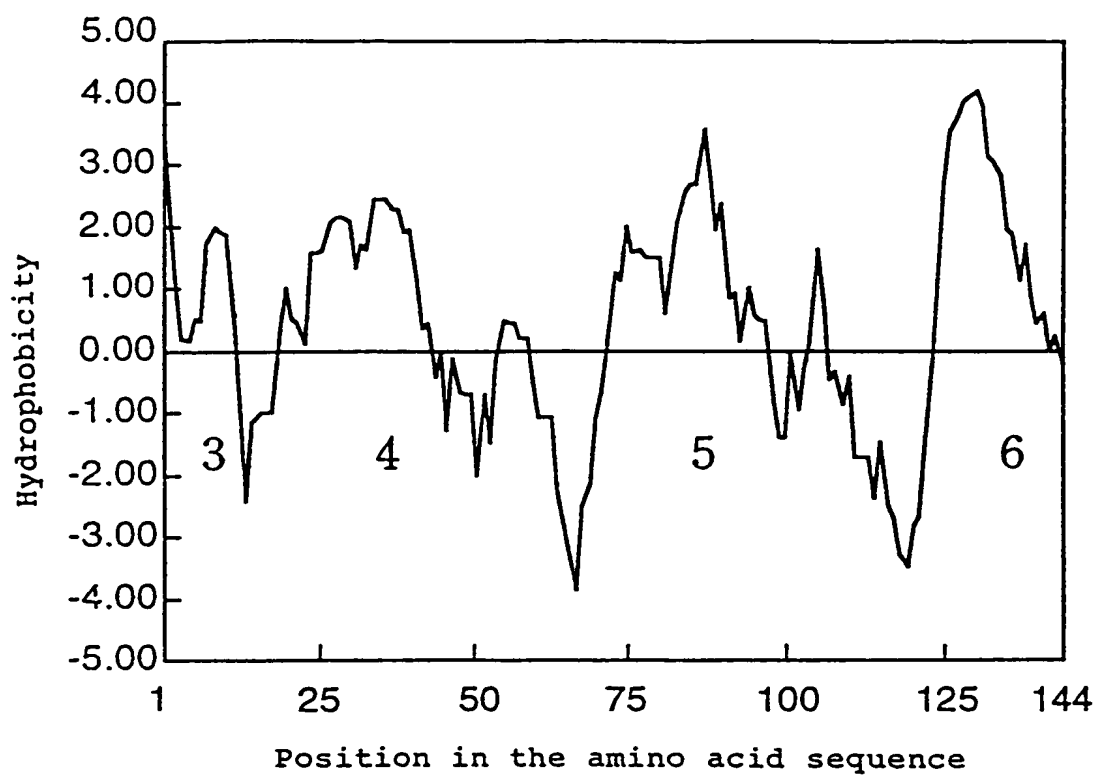


FIG. 14

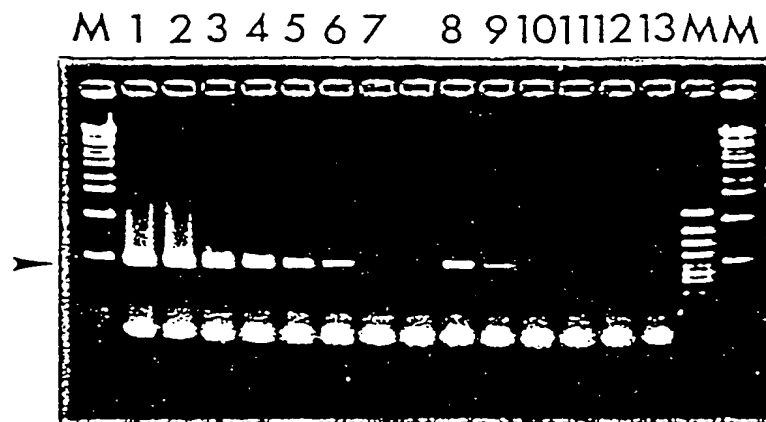


FIG. 15

19/60

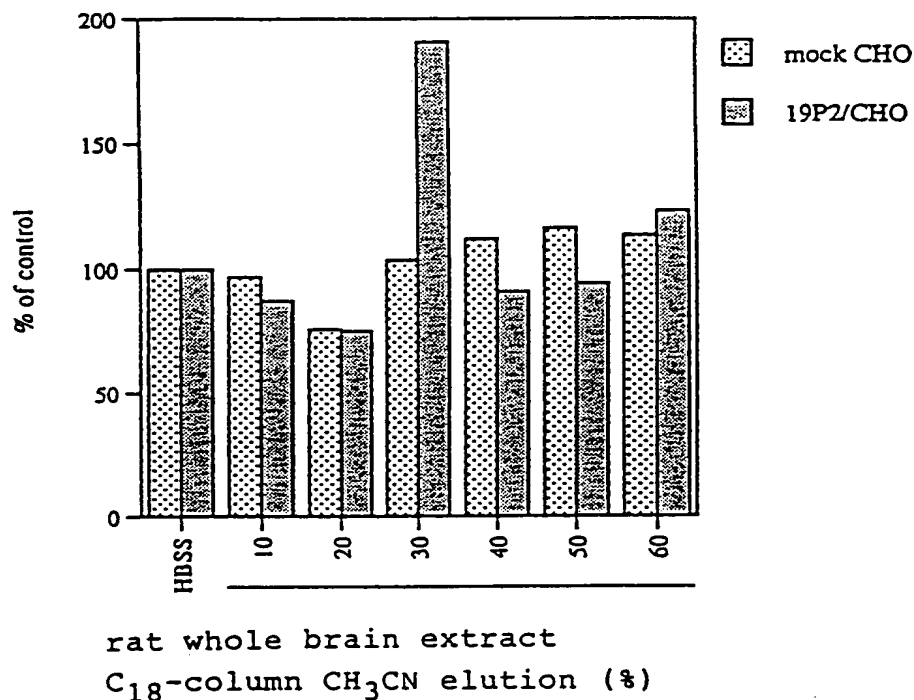


FIG. 16

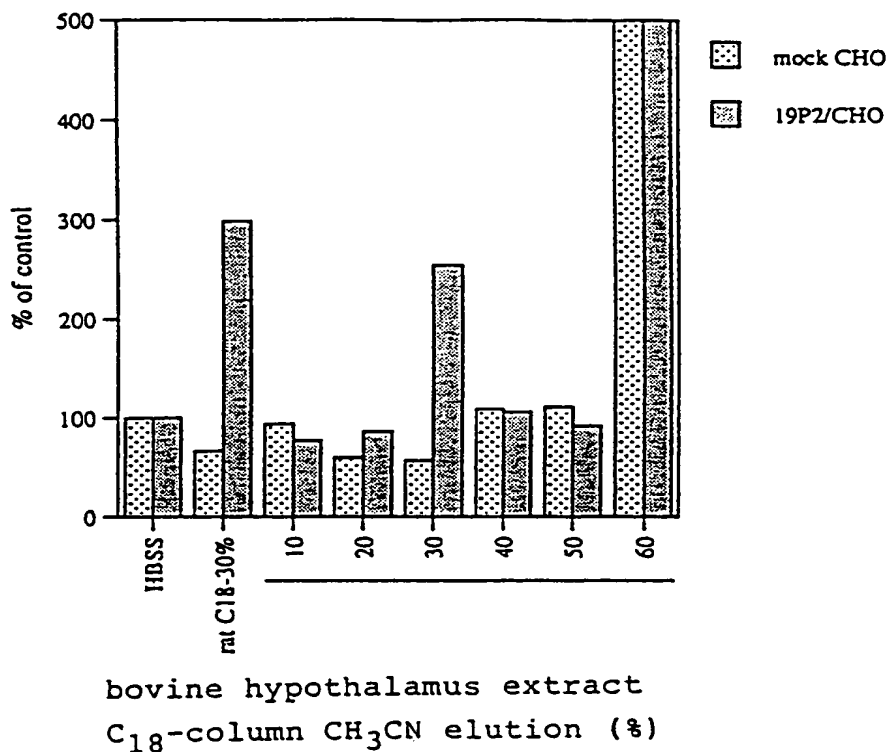


FIG. 17

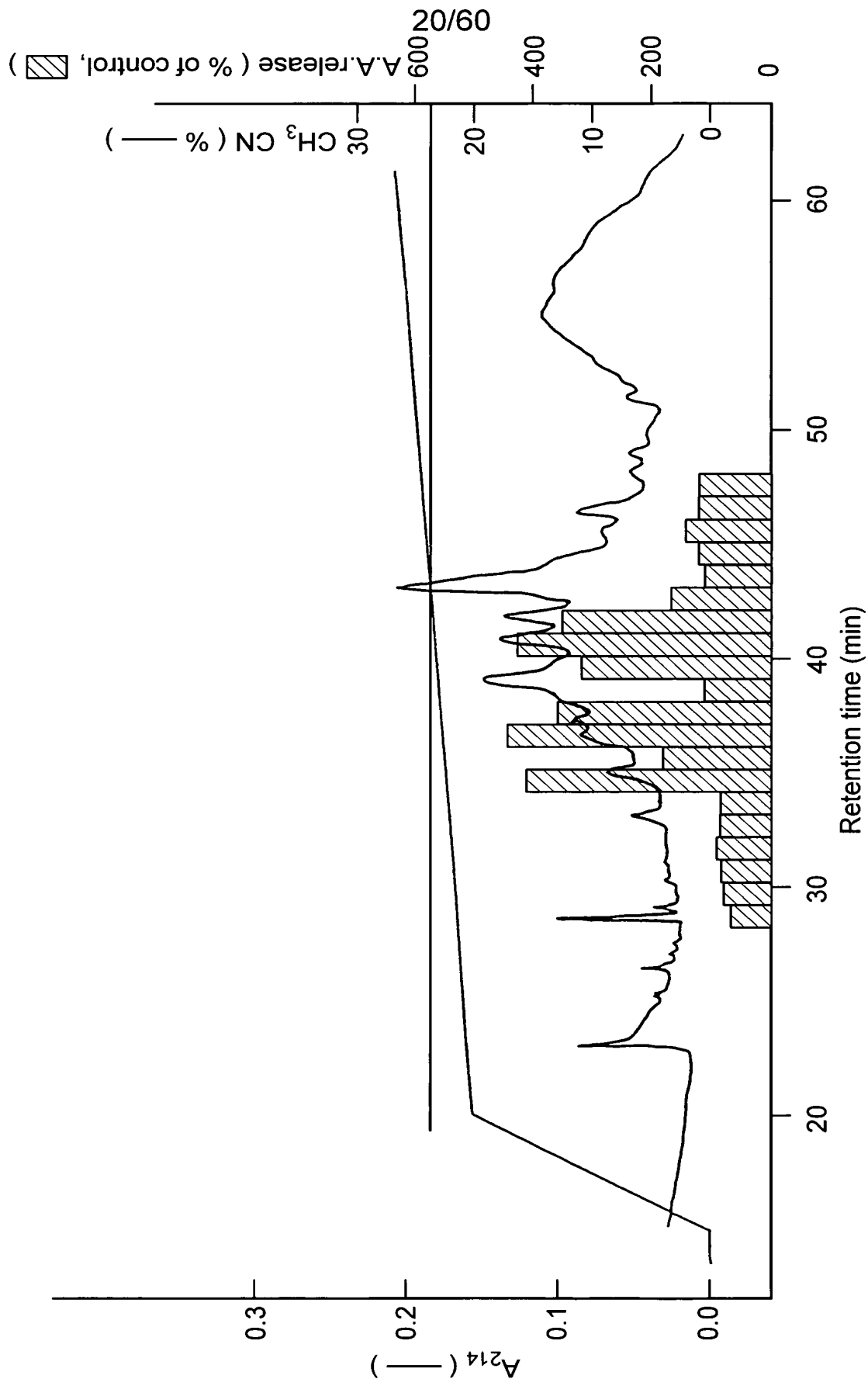
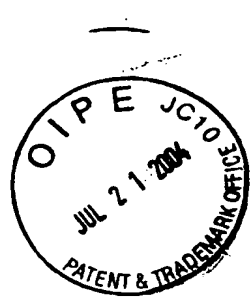


FIG. 18



21/60

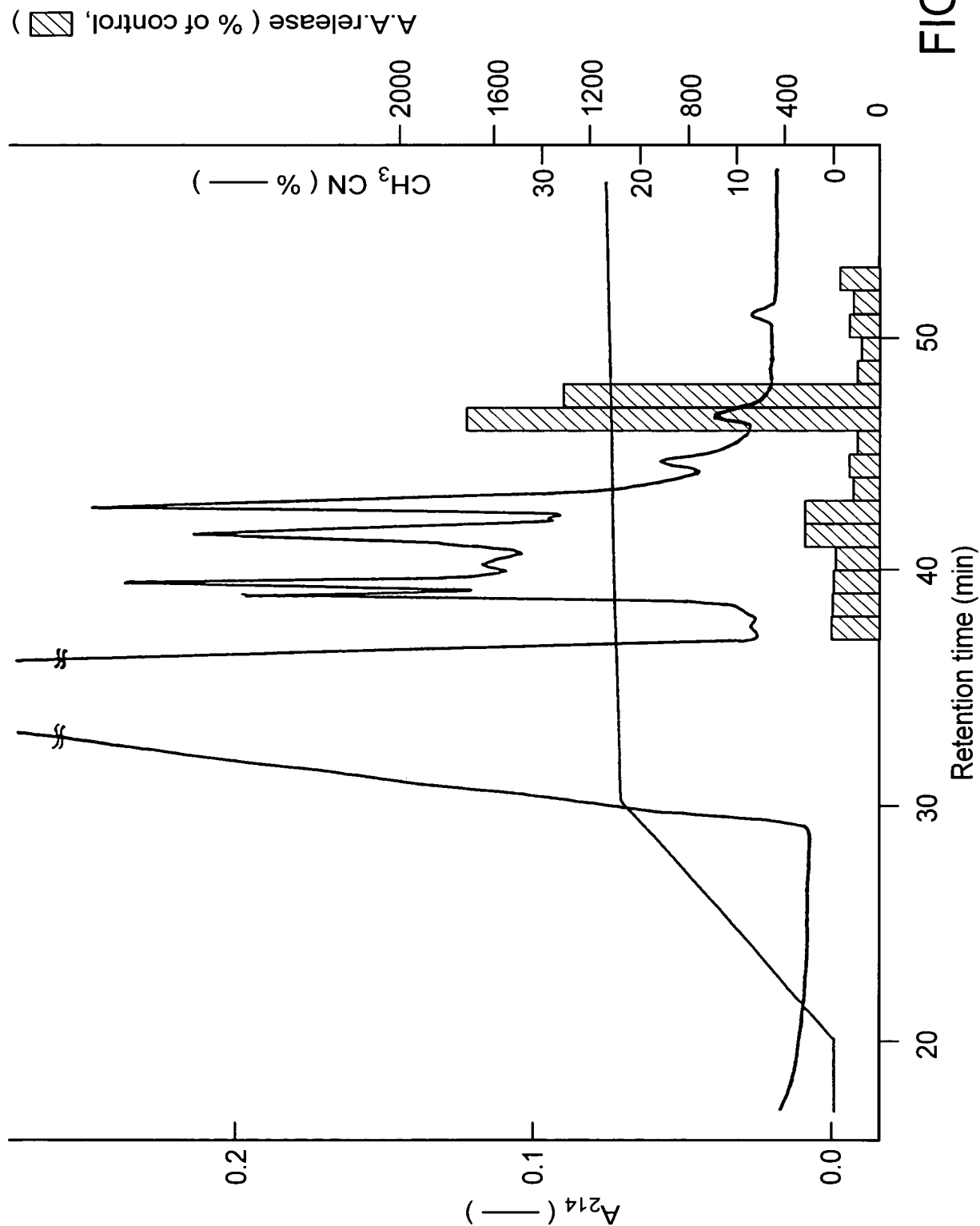
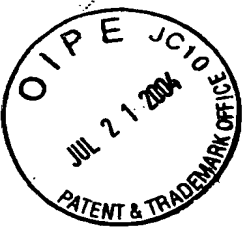
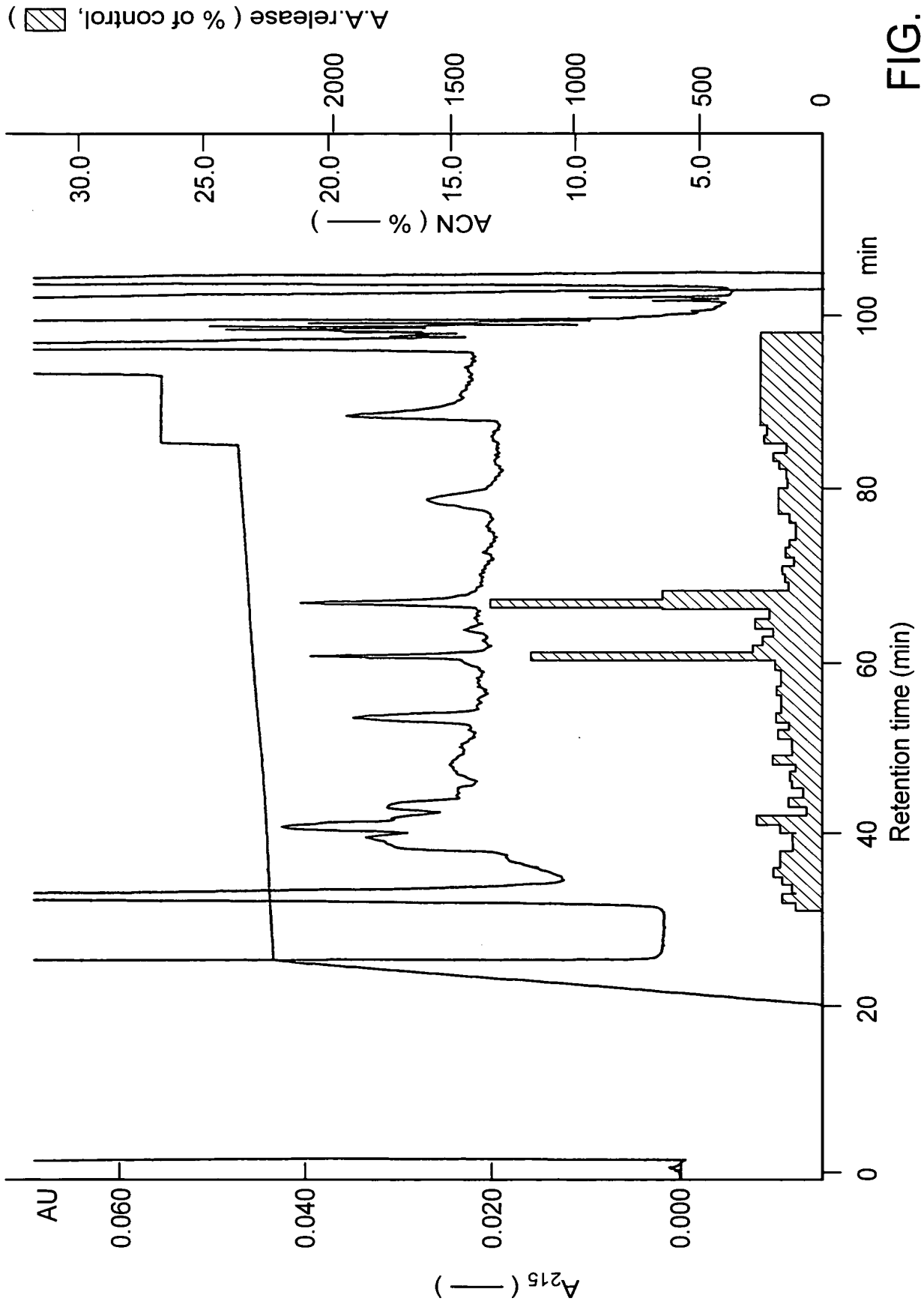


FIG. 19



22/60



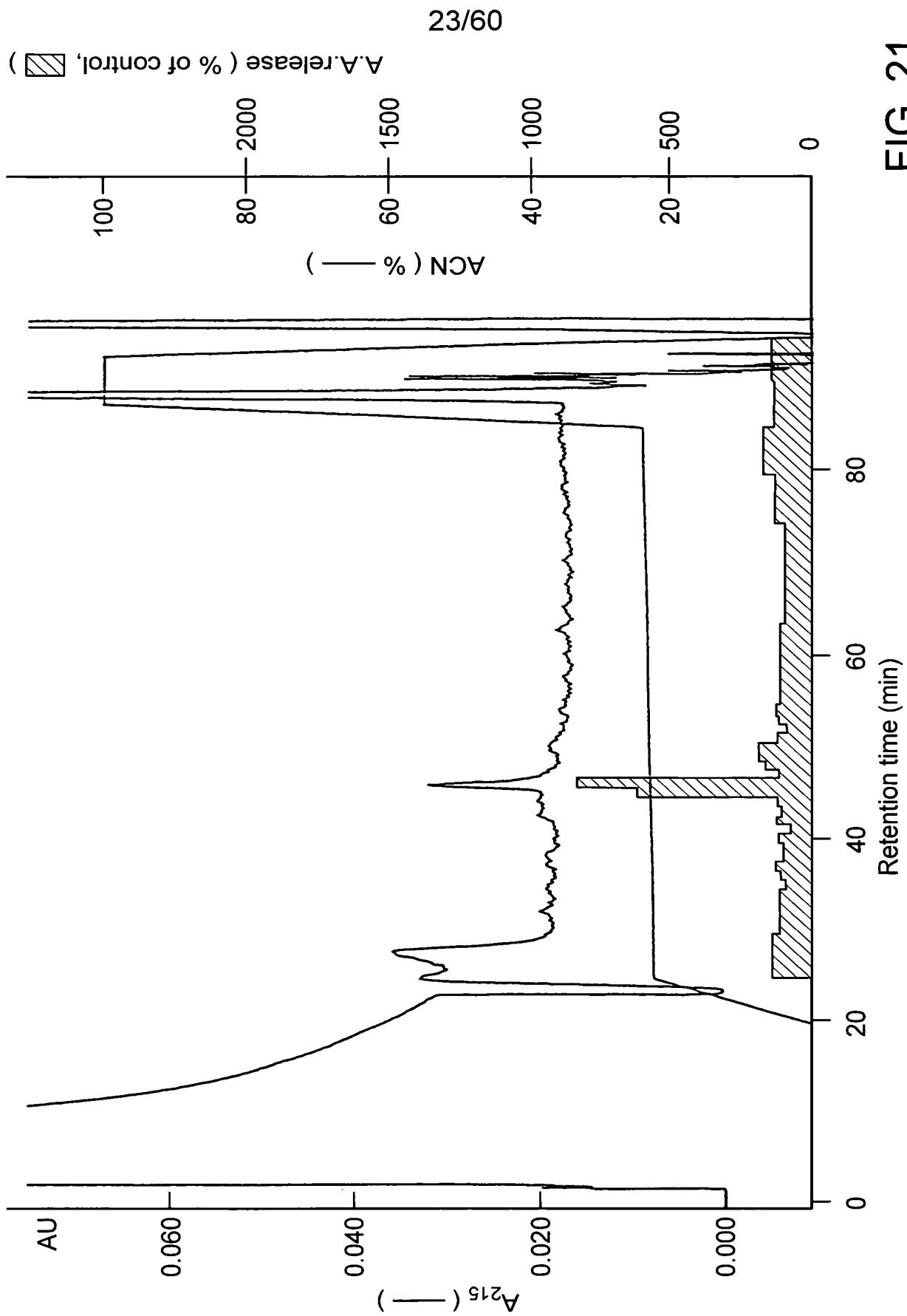
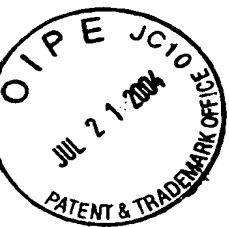
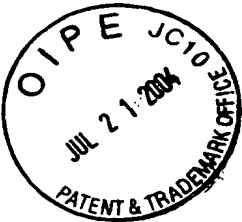


FIG. 21





P5-1

	9	18	27	36	45	54
5'	GCC CAC CAG CAC TCC ATG GAG ATC CGC ACC CCC GAC ATC AAC CCT GCC TGG TAC					
	---	---	---	---	---	---
	Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr					
						↓
	63	72				
	GGC GGC CGT GGG ATC CGG CCC G 3'					
	---	---	---	---	---	---
	Ala Gly Arg Gly Ile Arg Pro					

FIG. 22

P3-2

1	GTGGAATGAAGCGGTGGGGCCTGGCTCCTCTGCCTGCTGCTGGCCCTG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuGlyLeuAlaLeu	18
60	CAGGGGCTGCCAGAGCCACCAGCACTCCATGGAGATCCGCCACCCCGACATCAAC	119
19	GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn	38
	↓	
	PDN	
120	CCTGCCT	126
39	ProAla	40

FIG. 23

1	GTGGAATGAAGCGGTGGGGCCTGGCTCCTCTGCTGCTGCTGCTGGCCCTGGCCCTG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuGlyLeuAlaLeu	18
60	CAGGGGCTGCCAGCAGAGCCACAGCACTCCATGGAGATCCGCACCCCCGACATCAAC	119
19	GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn	38
120	CCTGCCTGTACGCRGGCCGTGGGATCCGGCCCCGTGGCCCGCTTCGGCCGGCGAAGAGCT	179
39	ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgArgAla	58
180	GGCCCCGGGACGGACCCAGGCCCTGGCCCCCGGGCGTGTGCCGGCCTGCTTCCGCCCTGGAA	239
59	AlaProGlyAspGlyProArgProGlyProArgValProAlaCysPheArgLeuGlu	78
240	GGCGGYGCTGAGCCCTCCCGAGCCCTCCCGGGGGGCTGACGGCCAGCTGGTCCAGGAA	299
79	GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu	98
300	TAAACAGGGAGCCTGCCCCCCCCCCTCCTCCTCCACCAGCCACCTTCCCCCAGTCCT	359
	98	98
360	AATAAAAGCAGCTGGCTTGTT	380
	98	98

FIG. 24A

1 GTGGAATGAAGCGGTGGGGCCTGGCTCCTCTGCTGCTGCTGGCCCTGGCCCTG 59  
1 MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuGlyLeuAlaLeu 18  
60 CAGGGGCTGCCAGCAGAGCCACCACTCCATGGAGATCCGCACCCCCGACATCAAC 119  
19 GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn 38  
120 CCTGCCTGGTACGCRGGCCGTGGGATCCGGCCCCGTGGCCCGCTTCGGCCGGCGAAGAGCT 179  
39 ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgAla 58  
180 GCCCTGGGGACGACCCAGGCCCTGGCCCCCGGCGTGTGCCGGCCTGCTTCCGCCCTGGAA 239  
59 AlaLeuGlyAspGlyProArgProGlyProArgValProAlaCysPheArgLeuGlu 78  
240 GCGGYGCTGAGCCCTCCCGAGCCCTCCCGGGGGCTGACGGCCCGAGCTGGTCCAGGAA 299  
79 GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu 98  
300 TAACAGCGGAGCCTGCCCCCACCCTCCTCCTCCACCAGCCACCTTCCCCCAGTCCT 359  
98  
360 AATAAAGCAGCTGGCTTGTT 380  
98

FIG. 24B

27/60

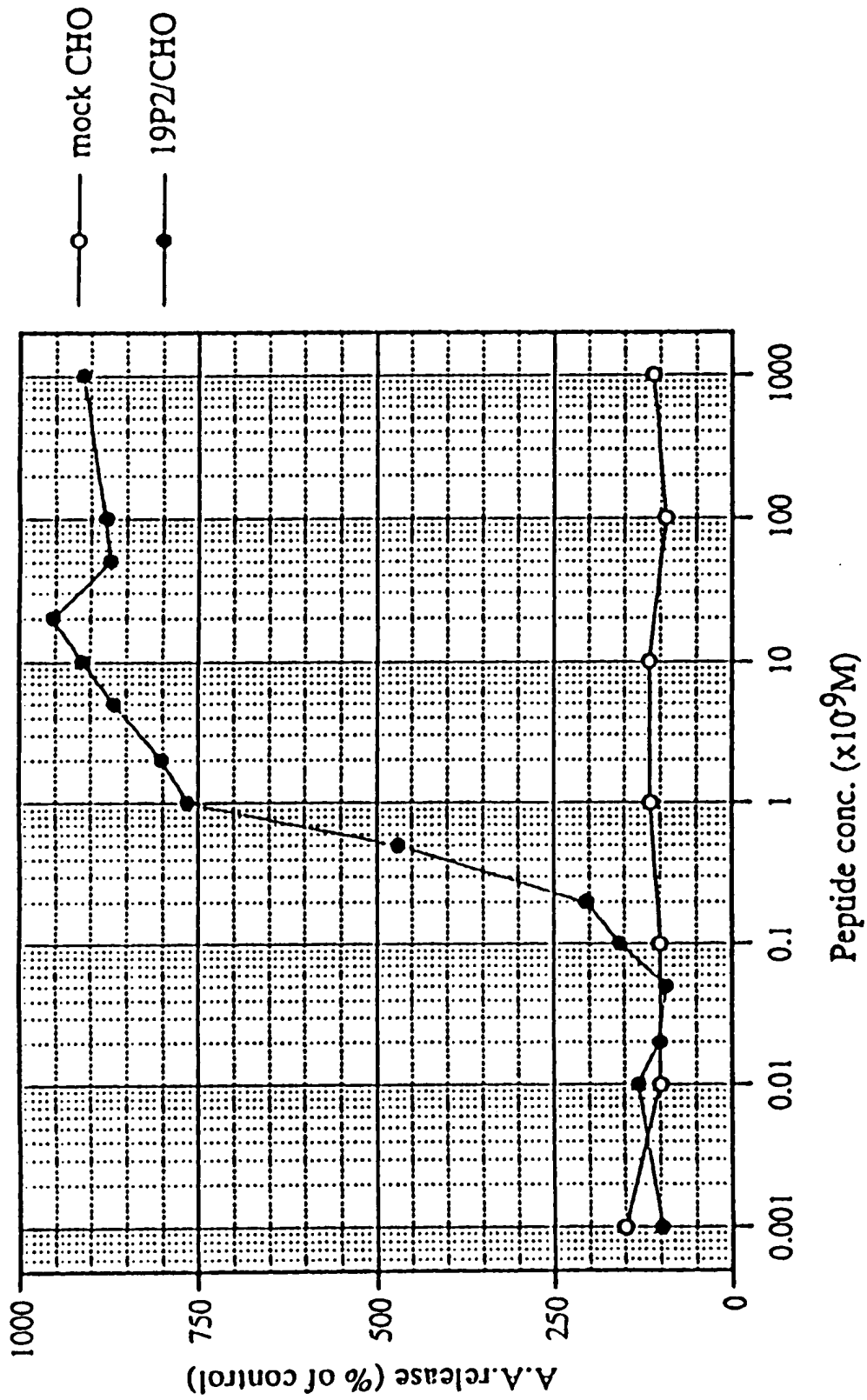


FIG. 25

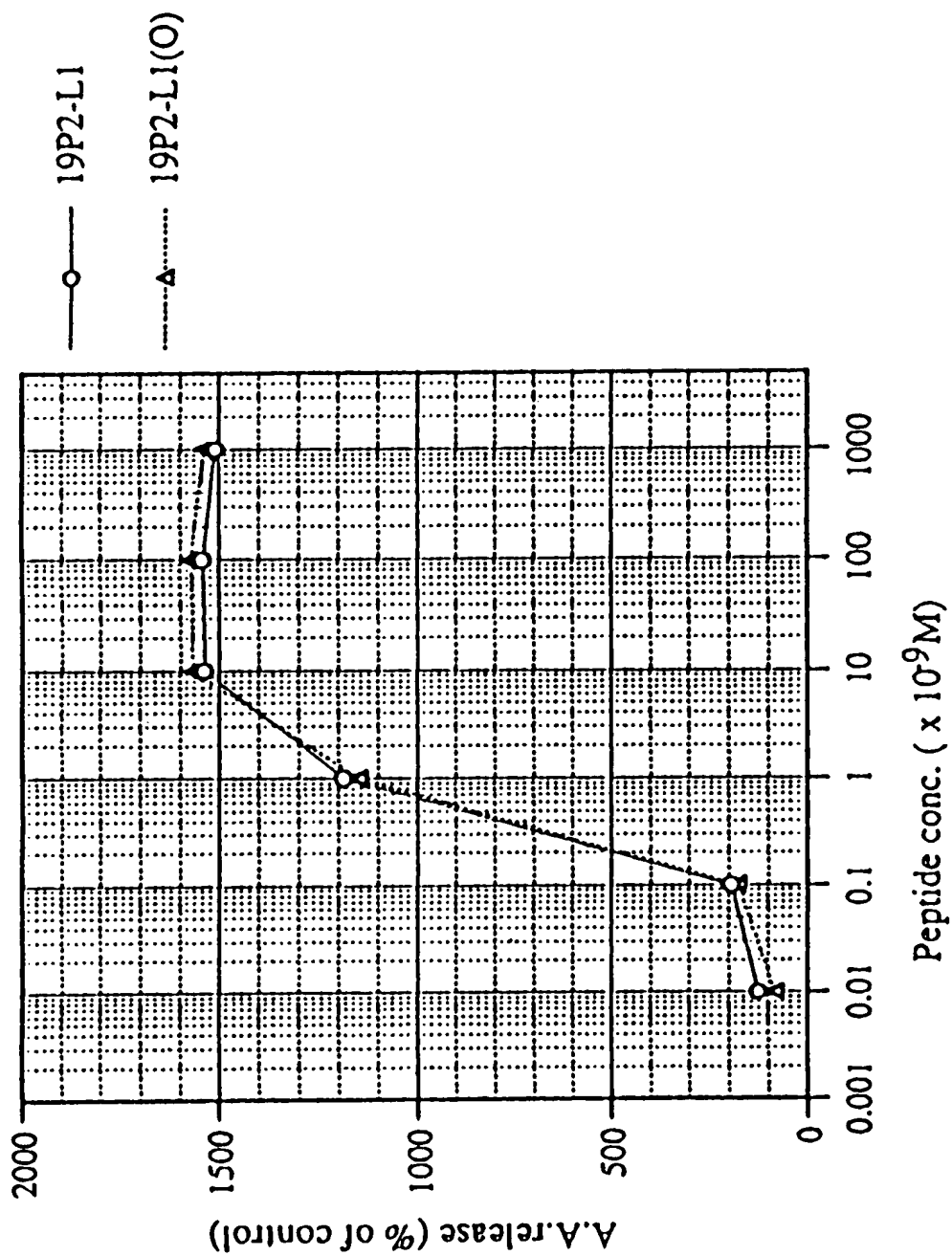


FIG. 26

29/60

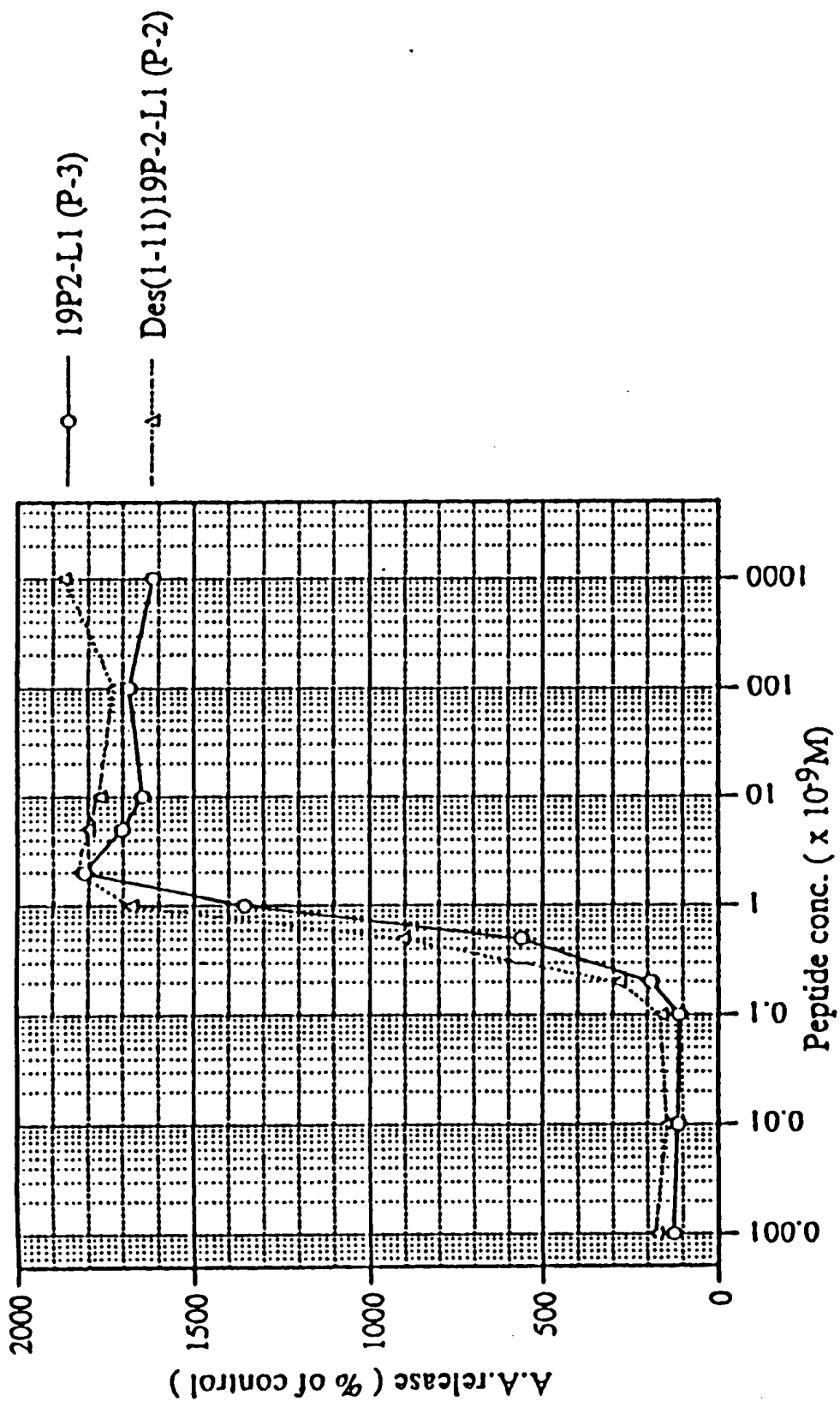


FIG. 27

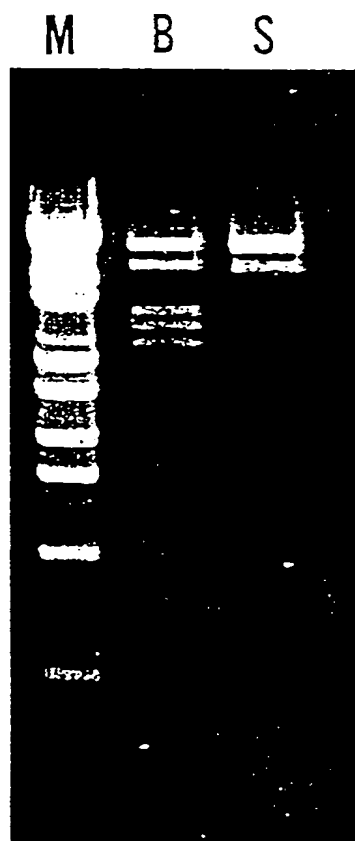
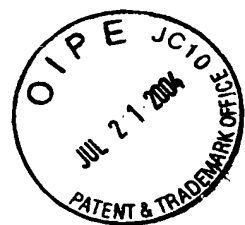


FIG. 28



31/60

10	20	30	40	50	60
ATGAAGGCGG	TGGGGGCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	CCTGCAGGGG
70	80	90	100	110	120
GCTGCCAGCA	GAGCCCAcca	GCACTCCATG	GAGATCCGCA	GTGAGTGTCT	AGCCCCGCCC
130	140	150	160	170	180
CTGCCCCCAG	GGGTCACAGG	GGGGGCCTGG	CCACTTCCTG	GGCTGGGACA	TCCTTGCTAA
190	200	210	220	230	240
GCATCCTGGG	GTGGGGGTTT	GGCCTCCTGT	TCCCCAGACC	CTTCCCCCAG	GTGGCCCCGA
250	260	270	280	290	300
CAGGTGCTCC	CAAGGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACTCCTC	ACCACACGGG
310	320	330	340	350	360
TGGCCTGGGG	CTGAGTGCAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	GGAAAGGAAG
370	380	390	400	410	420
GGGAGTGTGT	CCTGGTGTGA	GTCTGAAATC	CTACTTCCCA	AAGCCACCCC	AGCACCAGAA
430	440	450	460	470	480
ATGGGCGCTC	CGGGTGAACC	TCCTGTGCGG	GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA
490	500	510	520	530	540
GGCAGCCATG	AGCTGAGCAC	ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC
550	560	570	580	590	600
AGGCCTCCAT	GCGCTCTTCT	CTCTCTTTCC	AGCCCCCGAC	ATCAACCCTG	CCTGGTACGC
610	620	630	640	650	660
AGGCCGTGGG	ATCCGGCCCCG	TGGGCCGCTT	CGGCCGGCGA	AGAGCTGCCC	TGGGGGACGG
670	680	690	700	710	720
ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	CTGGAAGGCG	GTGCTGAGCC
730	740	750	760	770	780
CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	CCAGCTGGTC	CAGGAATAA.	.....

FIG. 29



FIG. 30A
FIG. 30B
FIG. 30C

FIG. 30

genome	1	ATGAAGCGG	10	TGGGGCCTG	20	GCTCCTCTG	30	CTGCTGCTG	40	TGGGCCTGGC	50
cDNA	1	ATGAAGCGG	10	TGGGGCCTG	20	GCTCCTCTG	30	CTGCTGCTG	40	TGGGCCTGGC	50
genome	51	CCTGCAGGG	60	GCTGCCAGCA	70	GAGCCACCA	80	GCACTCCATG	90	GAGATCCGCA	100
cDNA	51	CCTGCAGGG	60	GCTGCCAGCA	70	GAGCCACCA	80	GCACTCCATG	90	GAGATCCGCA	100
genome	101	GTGAGTGTCT	110	AGCCCCGCC	120	CTGCCCCCAG	130	GGTCACAGG	140	GGGGCCTGG	150
cDNA	101	GTGAGTGTCT	110	AGCCCCGCC	120	CTGCCCCCAG	130	GGTCACAGG	140	GGGGCCTGG	150
genome	151	CCACTTCCTG	160	GGCTGGGACA	170	TCCTTGCTAA	180	GCACTCCTGG	190	GTGGGGTTT	200
cDNA	151	CCACTTCCTG	160	GGCTGGGACA	170	TCCTTGCTAA	180	GCACTCCTGG	190	GTGGGGTTT	200

FIG. 30A

genome	201	210	220	230	240	250
cDNA	201	210	220	230	240	250
	GGCCTCCTGT	TCCCCAGACC	CTTCCCCCAG	GTGGCCCGGA	CAGGTGCTCC	
	-----	-----	-----	-----	-----	
genome	251	260	270	280	290	300
cDNA	251	260	270	280	290	300
	CAAGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACCTCCTC	ACCACACGGG	
	-----	-----	-----	-----	-----	
genome	301	310	320	330	340	350
cDNA	301	310	320	330	340	350
	TGGCCTGGGG	CTGAGTGCAC	GTCACCCCATG	AGAACGGGGC	TGTGAGGACA	
	-----	-----	-----	-----	-----	
genome	351	360	370	380	390	400
cDNA	351	360	370	380	390	400
	GGAAAGGAAG	GGGAGTGTGT	CCTGGTGTGA	GTCTGAATC	CTACTTCCCA	
	-----	-----	-----	-----	-----	
genome	401	410	420	430	440	450
cDNA	401	410	420	430	440	450
	AAGCCACCCC	AGCACCAGAA	ATGGGGCGCTC	CGGGTGAACC	TCCTGTGCGG	
	-----	-----	-----	-----	-----	
genome	451	460	470	480	490	500
cDNA	451	460	470	480	490	500
	GTGGGTGGTC	CTGGCATGGC	CTGGGGGACA	GGCAGCCATG	AGCTGAGCAC	
	-----	-----	-----	-----	-----	

FIG. 30B



genome cDNA	501	510	520	530	540	550
	ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC	AGGCCTCCAT	
501	-----	-----	-----	-----	-----	-----
genome cDNA	551	560	570	580	590	600
	GCGCTCTTCT	CTCTCTTTCC	AGCCCCCGAC	ATCAACCCCTG	CCTGGTACGC	
551	-----	-----	-----	ATCAACCCCTG	CCTGGTACGC	
genome cDNA	601	610	620	630	640	650
	AGGCCGTGGG	ATCCGGGCCC	TGGCCCGCTT	CGGCCGGCGA	AGAGCTGCCC	
601	GGGCCGTGGG	ATCCGGGCCC	TGGCCCGCTT	CGGCCGGCGA	AGAGCTGCCC	
genome cDNA	651	660	670	680	690	700
	TGGGGACGG	ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	
651	CGGGGACGG	ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	
genome cDNA	701	710	720	730	740	750
	CTGGAAGCG	GTGCTGAGCC	CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	
701	CTGGAAGCG	GGCTGAGCC	CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	
genome cDNA	751	760	770	780	790	800
	CCAGCTGGTC	CAGGAATAA.	.....	.....	.....	
751	CCAGCTGGTC	CAGGAATAA.	.....	.....	.....	

FIG. 30C

5'	9	18	27	36	45	54
ATG AAG GCG GTG GGG GCC TGG CTC CTC TGC CTG CTG GGC CTG GCC CTG						
M K A V G A W L L C L L L G L A L						
63	72	81	90	99	108	
CAG GGG GCT GCC AGC AGA GCC CAC CAG CAC TCC ATG GAG ATC CGC ACC CCC GAC						
Q G A A S R A H Q H S M E I R T P D						
117	126	135	144	153	162	
ATC AAC CCT GCC TGG TAC GCA GGC CGT GGC ATC CGG CCC GTG GGC CGC TTC GGC						
I N P A W Y A G R G I R P V G R F G						
171	180	189	198	207	216	
CGG CGA AGA GCT GCC CTG GCG GAC GGA CCC AGG CCT GGC CCC CGC CGT GTG CCG						
R R R A A L G D G P R P G P R R V P						
225	234	243	252	261	270	
GCC TGC TTC CGC CTG GAA GGC GGT GCT GCT GAG CCC TCC CGA GCC CTC CCG GGG CCG						
A C F R L E G G A E P S R A L P G R						
279	288	297				
CTG ACG GCC CAG CTG GTC CAG GAA TAA 3'						
L T A Q L V Q E *						

FIG. 31

1 GGCAATCATCCAGGAAGACGGAGCATGGCCCTGAAGACGTGGCTTCTGTGCTTGCTGCTG 59  
1 MetAlaLeuLysThrTrpLeuLeuCysLeuLeuLeu 12  
1  
60 CTAAGCTTGGTCCCTCCAGGGGCTTCAGCCGAGCCACCCAGCACTCCATGGAGACAAGA 119  
13 LeuSerLeuValLeuProGlyAlaSerSerArgAlaHisGlnHisSerMetGluThrArg 32  
120 ACCCCTGATATCAATCCTGCCTGGTACACGGGCCCGGGATCAGGCCCTGTGGCCGCTTC 179  
33 ThrProAspIleAsnProAlaTrpTyrThrGlyArgGlyIleArgProValGlyArgPhe 52  
180 GGCAGGAGAAGGCAACCCGAGGGATGTCACTGGACTTGGCCAACTCAGCTGCCTCCCA 239  
53 GlyArgArgArgAlaThrProArgAspValThrGlyLeuGlyGlnLeuSerCysLeuPro 72  
240 CTGGATGGACGCACCAAGTTCTCTCAGCGTGGATAACACCCAGCTCGAGAAGACAGTGC 299  
73 LeuAspGlyArgThrLysPheSerGlnArgGly\*\*\* 83  
300 TGCTGAGCCCAAGCCCACTCCCCTGTCCCCTGCAGACCCCTCCTCTACCCCTCCCTCCT 359  
83 83  
360 CTGCT 364  
83 83

36/60

FIG. 32

		M	K	A	V	G	A	W	L	L	
	10			20			40			50	
-18	.....	GT	GGAATGAAGG	CGGTGGGGGC	CTGGCTCCTC						32
1	GGCATCATCC	AGGAAGACGG	AGCATG---	G CCTGAAGAC	GTGGCTTCIG						50

-18 .....GT GGAATGAAGG CGGTGGGGGC CTGGCTCCTC 32  
1 GGCATCATCC AGGAAGACGG AGCATG---G CCTGAAGAC GTGGCTTCTG 50

8 .....GT GGAATGAAGG CCGTGGGGGC CTGGCTCCTC 32  
1 GGCATCATCC AGGAAGACGG AGCATG---G CCCTGAAGAC GTGGCTTCTG 50

C	L	L	L	L	G	L	A	L	Q	G	A	S	R	A	H
				60			70		80			90			100

33 TGCCTGCTGC TCCTGGGCTT GGGCTGCTGAG GGGGCTGCCA GCAGAGCCCC 82

51 TGCCTGCTGC TGCTAAGCTT GTCTCTCCCA GGGGCTTCCA GCGGAGCCCC 100

R1

33 TGCCTGCTGC TCCTGGGCTT GGGCTGCTGAG GGGGCTGCCA GCAGAGCCCC 82

51 TGCCTGCTGC TGCTAAGCTT GTCTCTCCCA GGGGCTTCCA GCGGAGCCCC 100

R1

	Q	H	S	M	E	I	R	T	P	D	I	N	P	A	W	Y	A	
			110			120			130			140		150				
83	CCAGCACTCC	ATGGAGATCC	GCACCCCCGA	CATCAACCCT	GCCTGTTACG													132
101	CCAGCACTCC	ATGGAGACAA	GAACCCCTGA	TATCAATCCT	GCCTGTTACA													150

R3

83 CCAGCACTCC ATGGAGATCC GCACCCCGA CATCAACCCT GCCTGGTAGG 132  
 101 CCAGCACTCC ATGGAGACAA GAACCCCTGA TATCAATCCT GCCTCGTACA 150  
 R3

83 CCAGCACTCC ATGGAGATCC GCACCCCGA CATCAACCCT GCCTGGTAGG 132  
 101 CCAGCACTCC ATGGAGACAA GAACCCCTGA TATCAATCCT GCCTCGTACA 150  
 R3

G R G I R P V G R F G R R A A  
 160 170 180 190 200  
 133 CGGGCCGTGG GATCCGGCCC GTGGGCGGCT TCGGCCGGCG AAGAGCTGCC 182  
 151 CGGGCCGGG GATCAGGCCT GTGGGCGGCT TCGGCAGGAG AAGGCAACC 200

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539 888  
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595 1000  
596 1002  
597 1004  
598 1006  
599 1008  
600 1010  
601 1012  
602 1014  
603 1016  
604 1018  
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621 1052  
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625 1060  
626 1062  
627 1064  
628 1066  
629 1068  
630 1070  
631 1072  
632 1074  
633 1076  
634 1078  
635 1080  
636 1082  
63

37/60

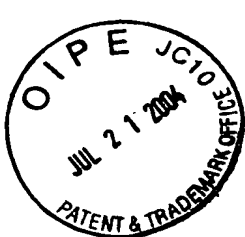
bovine.aa	P G D G P R P G P R R V P A C F R	
	210 220 230 240 250	
bovine.seq	183 CCGGGGACG GACCCAGGC TGGCCCCCGG CGTGTCGGG CCTGCTMCCG	232
rat.seq	201 CCGAGGGATG TCACTGGACT TGGC-----CAACTCA CCTGCCCTGCC	250
bovine.aa	L E G G A E P S R A L P G R L T A	
	260 270 280 290 300	
bovine.seq	233 CCTGGAAGGC GGCCTGAGC CTTCCCGAGC CTTCCCGGG CCGCTGACGG	282
rat.seq	251 ACTGGATGGA CGACCAAGT TCTCTCAGCG TGGATAACAC CCCAGCTCGA	300
bovine.aa	Q L V Q E *	
	310 320 330 340 350	
bovine.seq	283 CCCAGCTGGT CCAGGAATAA CAGCGGAGC CTGCCCCCCA CCCCCTCTCC	332
rat.seq	301 GAAGACAGTG CTGCTGAGCC CAAGCCCACA CTCCCTGTCC CCTGCAGACC	350
	360 370 380 390 400	
bovine.seq	333 TCCACCAGCC ACCTTCCCTC CAGTCCTAAT AAAAGCAGCT GGCTTGT...	382
rat.seq	351 CTCCTCTACC CTCCTCTCC TCIGT.....	400

FIG. 33B

1 GGCCTCCTCGGAGGAGCC AAGGATGAAGTGCTGAGGGCCTGGCTCCTGTGCCTGCTG 59  
12 MetLysValLeuArgAlaTrpLeuLeuCysLeuLeu  
60 ATGCTGGGCCCTGGCCCTGCGGGAGCTGCAAGTCGTACCCATCGGCACCTCCATGGAGATC 119  
32 MetLeuGlyLeuAlaLeuArgGlyAlaAlaSerArgThrHisArgHisSerMetGluIle  
120 CGCACCCCTGACATCAATCCTGCCTGGTACGCCAGTCGCGGGATCAGGCCCTGTGGGCCCGC 179  
52 ArgThrProAspIleAsnProAlaTrpTyrAlaSerArgGlyIleArgProValGlyArg  
239 TTCGGTCGGAGGGCAACCCCTGGGGGACGTCCCCAAGCCTGGCCTGCGACCCCGGCTG 239  
72 PheGlyArgArgAlaThrLeuGlyAspValProLysProGlyLeuArgProArgLeu  
299 ACCTGCTTCCCCCTGGAAGCGGTGCTATGTCGTCCCAGGATGGCTGACAGCCAGCCTTGT 299  
87 ThrCysPheProLeuGluGlyGlyAlaMetSerSerGlnAspGly\*\*\*  
300 CAAGAAACTCACTCTGGAGCCTCCCCCACCCTCTCCTCTCCTCTCGGGCTCCTTTC 359  
87  
360 CC 361  
87

FIG. 34





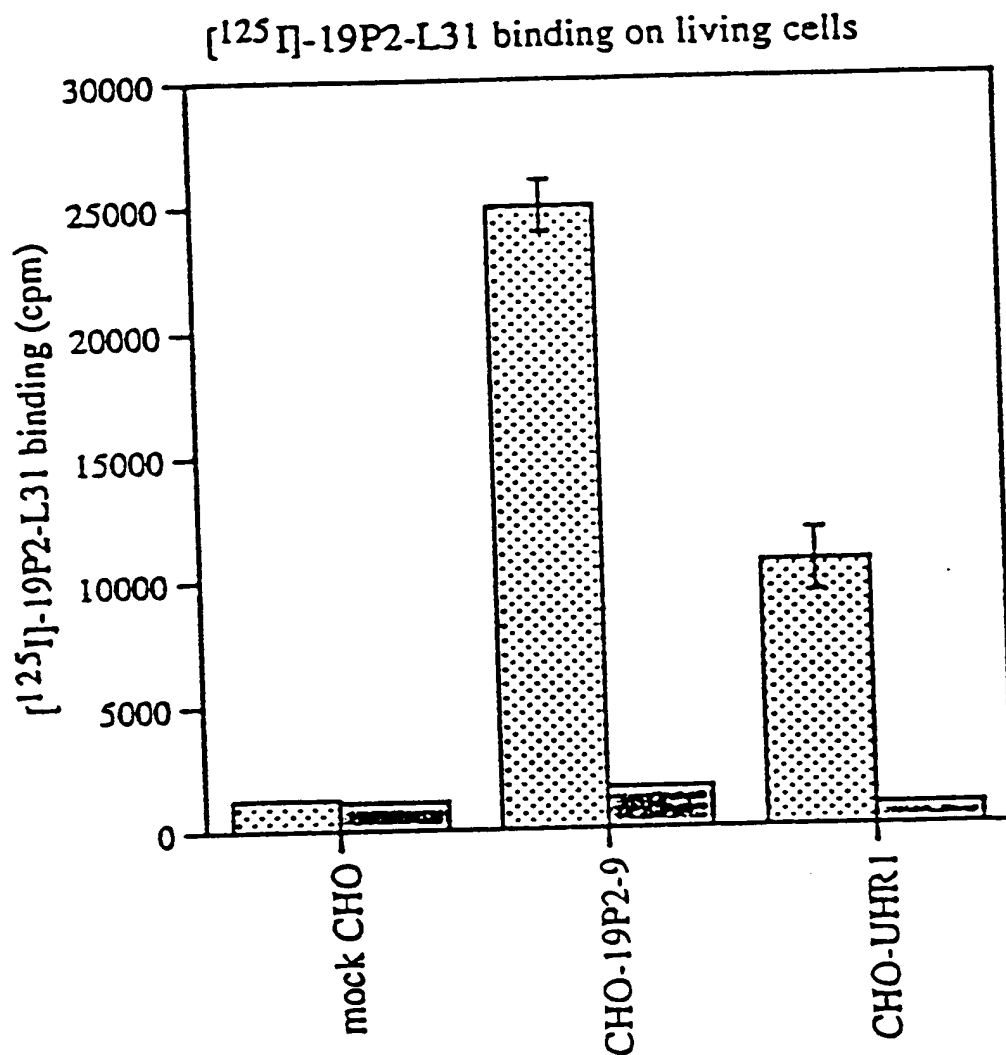
	10	20	30	40	50	
bovine.aa	1 MKAVGAWLLC	LLLLGLALQG	AASRAHQHSM	EIRTPDINPA	WYAGRGIRFV	50
rat.aa	1 M-ALKTWLLC	LLLLSLVLPG	ASSRAHQHSM	ETRTPDINPA	WYTGGRGIRFV	50
human.aa	1 MKVLRWLLC	LLMLGLALRG	AASRTHRHSM	EIRTPDINPA	WYASRGIRFV	50
bovine.aa	51 GRFGRRRAAP	GDGFRFGPRR	VPACFRLEGG	AEPSRALPCR	LTAQLVQE*	100
rat.aa	51 GRFGRRRATP	RDTVGLG---	QLSCLPLDGR	TKFSQRG*	.....	100
human.aa	51 GRFGRRRATL	GDVFKFGLRP	RLTCEPLEGG	AMSSQDG*	.....	100

40/60

FIG. 35

▨ Total binding

▨ NSB



cells;  $0.5 \times 10^7$  cells/ml

[<sup>125</sup>I]-19P2-L31; 200pM (avg. 63857.3cpm)

NSB; 200nM (x 1,000)

reaction; RT, 2.5hr

in HBSS + 0.05% BSA + 0.05% CHAPS

in 100  $\mu$ l

FIG. 36

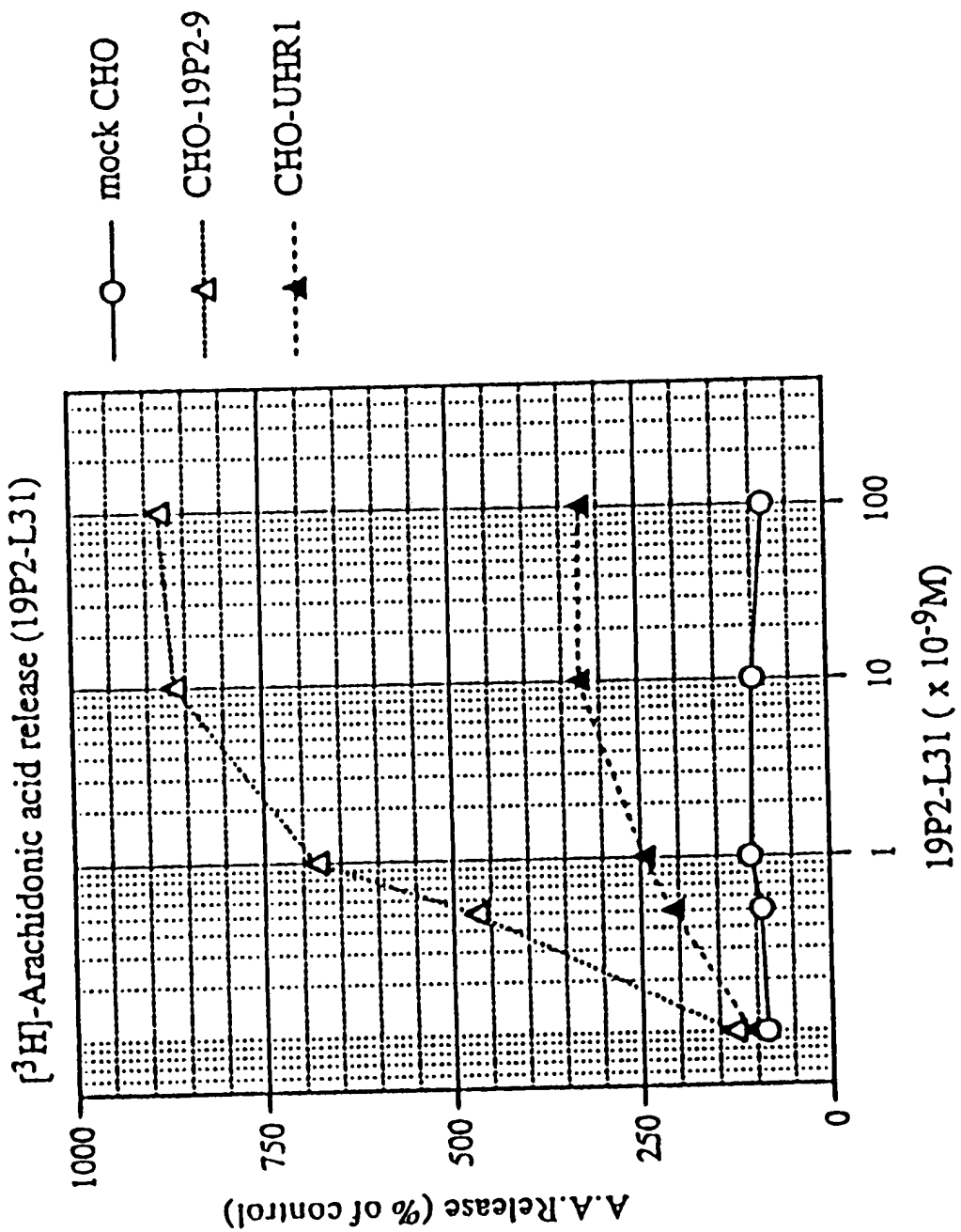


FIG. 37

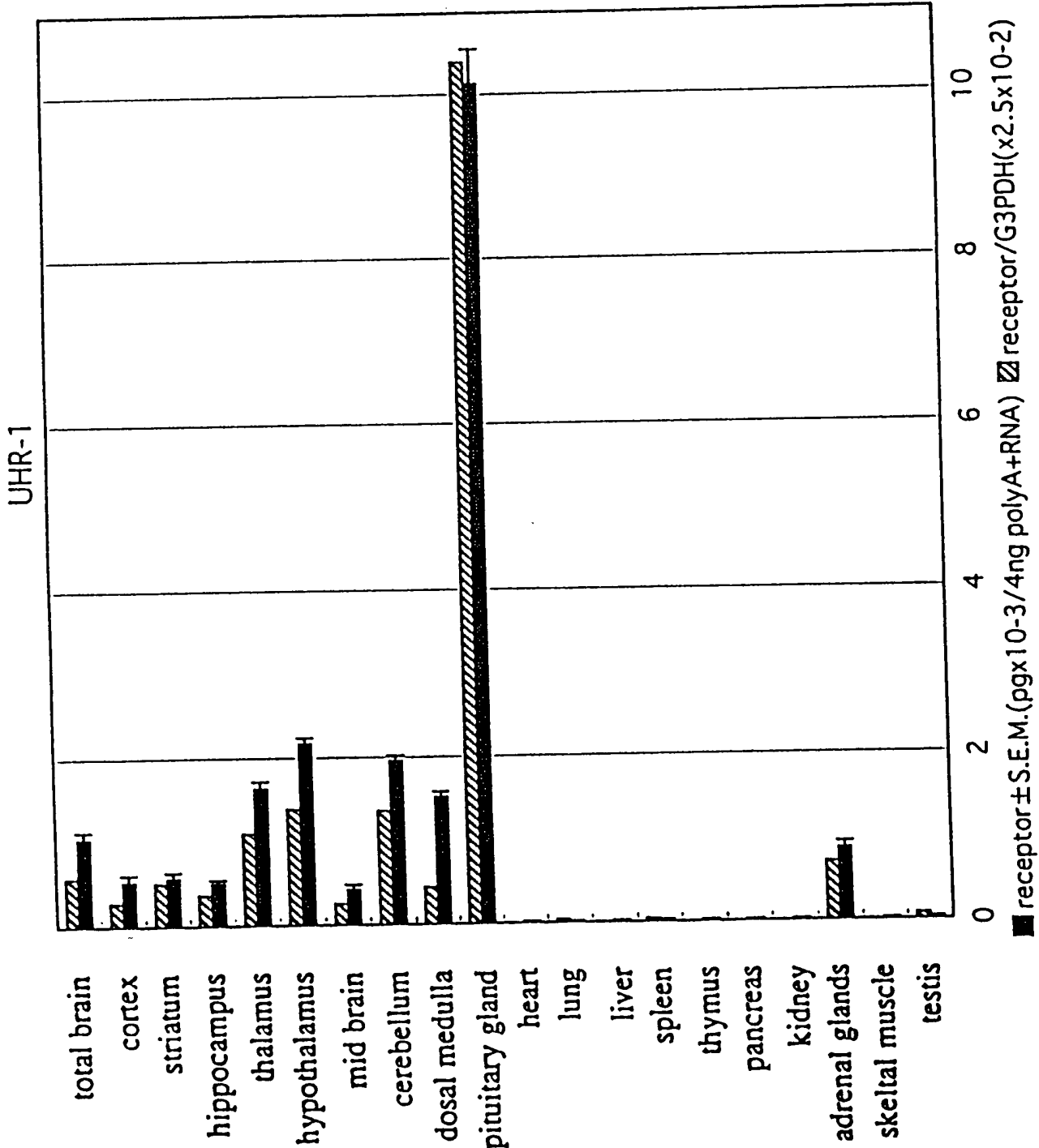
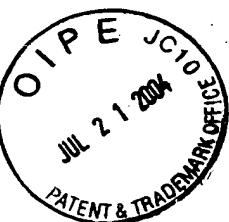


FIG. 38

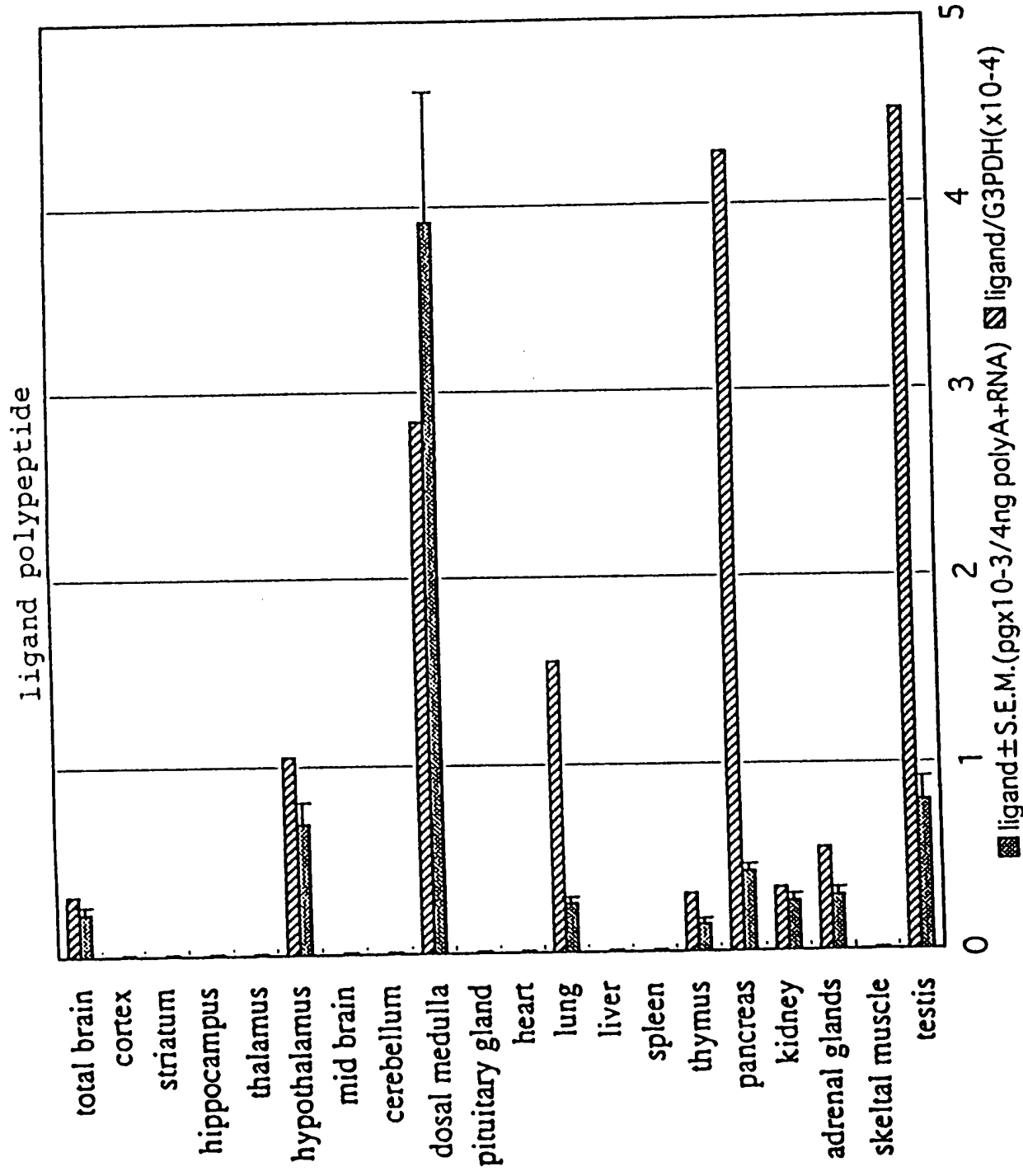


FIG. 39

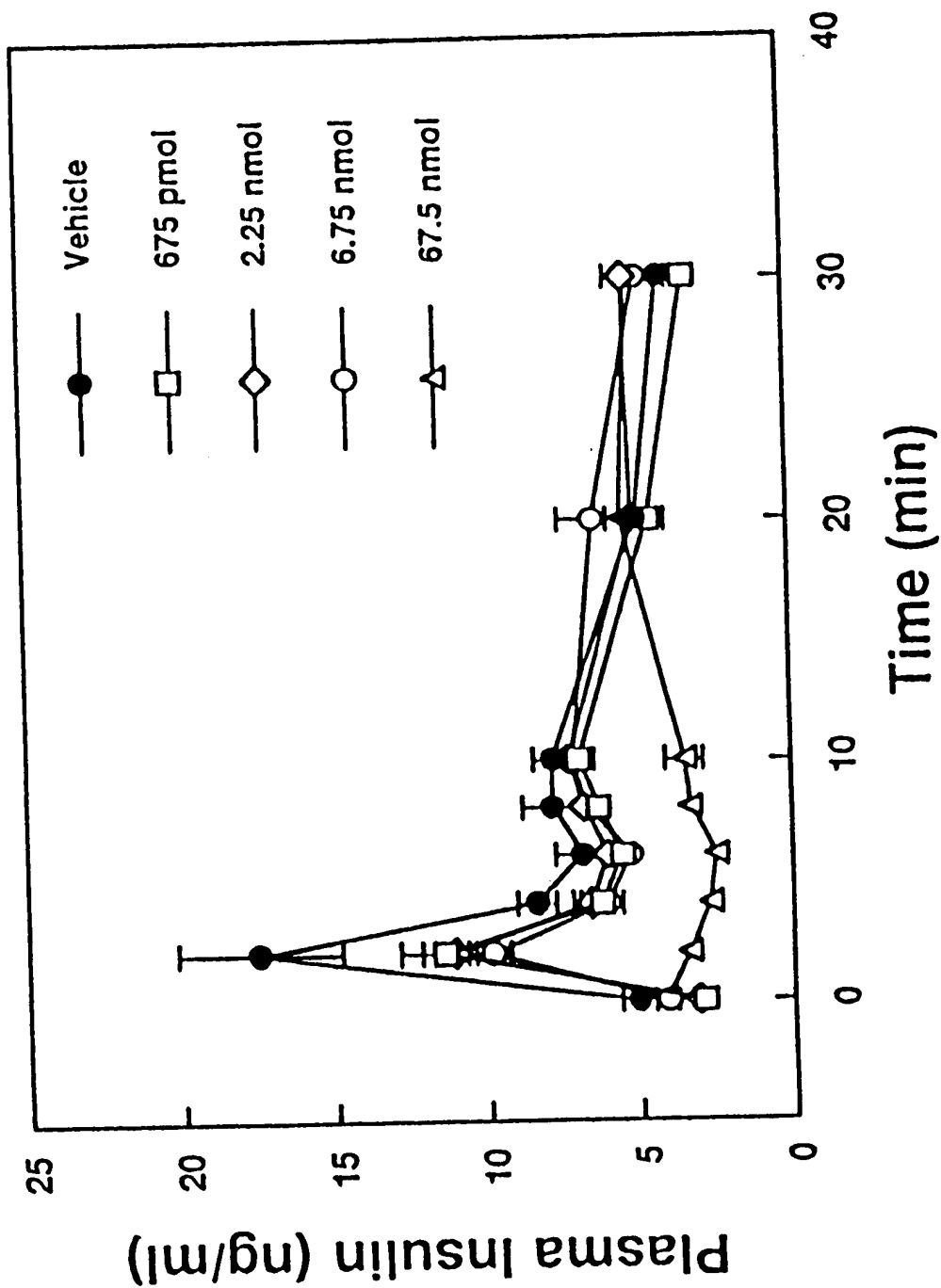


FIG. 40

46/60

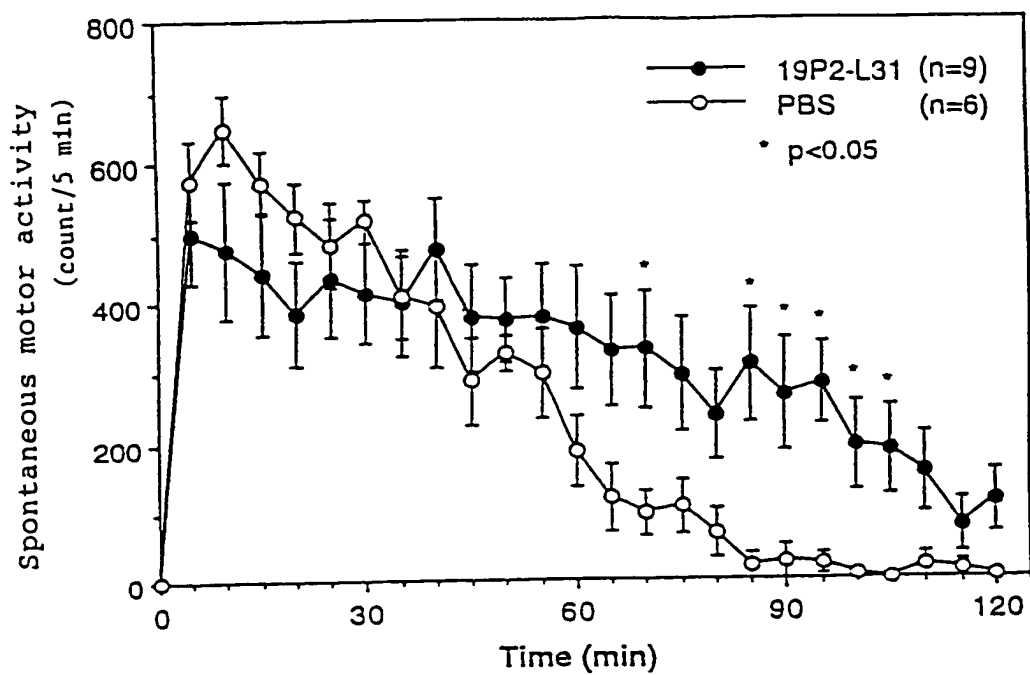


FIG. 41A

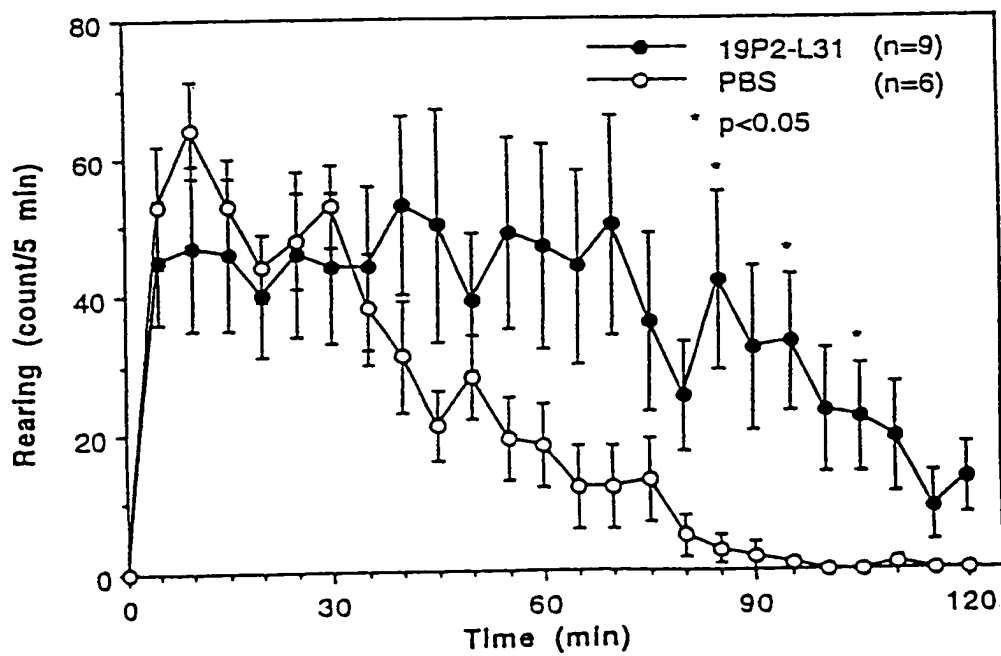


FIG. 41B

47/60

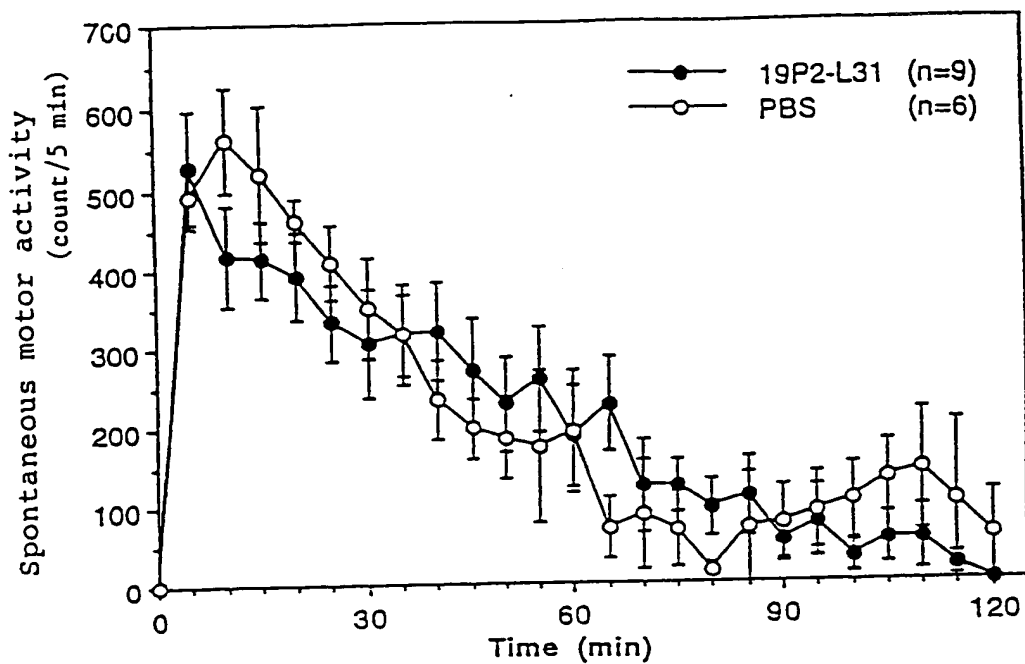


FIG. 42A

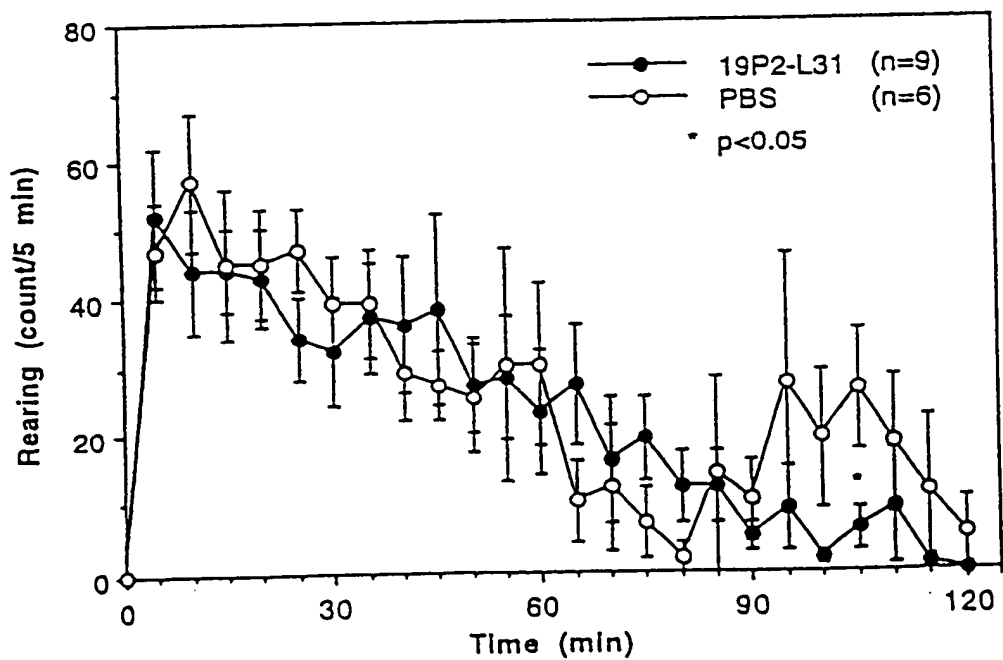


FIG. 42B



Figure 1 is a line graph showing spontaneous motor activity (count/5 min) on the y-axis (0 to 800) versus time (min) on the x-axis (0 to 120). Two groups are compared: 19P2-L31 (n=9, solid line with filled circles) and PBS (n=6, solid line with open circles). Error bars represent standard error. Asterisks (\*) indicate p < 0.05.

Time (min)	19P2-L31 (count/5 min)	PBS (count/5 min)
0	0	0
5	580	520
10	530	450
15	480	360
20	480	330
25	430	240
30	320	200
35	320	150
40	310	120
45	210	130
50	120	60
55	120	40
60	60	20
65	100	20
70	80	20
75	30	40
80	40	60
85	40	40
90	40	60
95	50	40
100	40	30
105	50	50
110	60	110
115	50	100
120	40	100

49/60

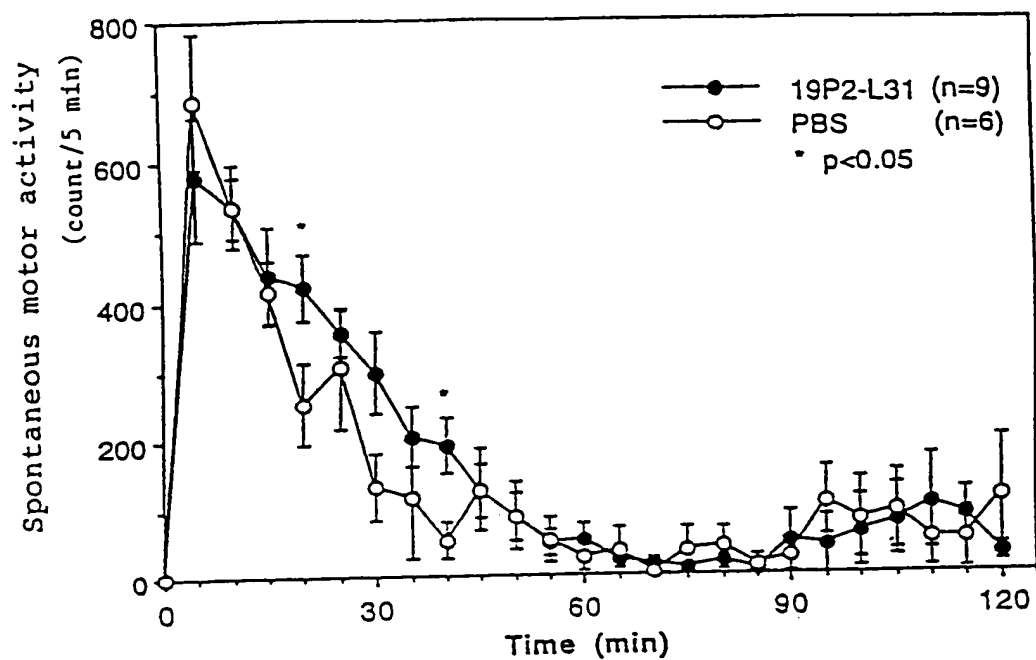


FIG. 44A

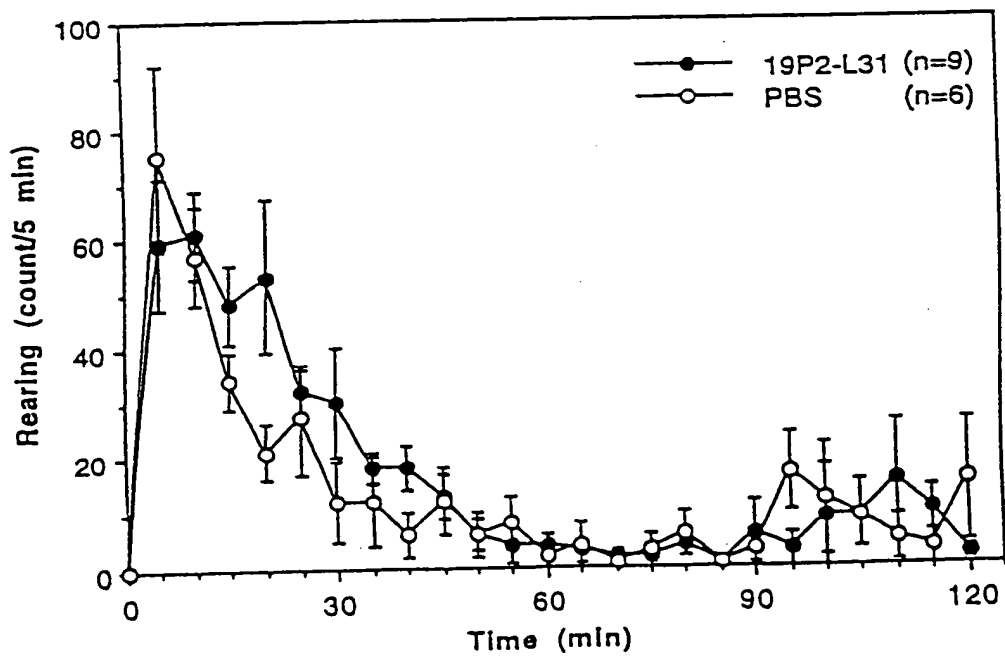


FIG. 44B

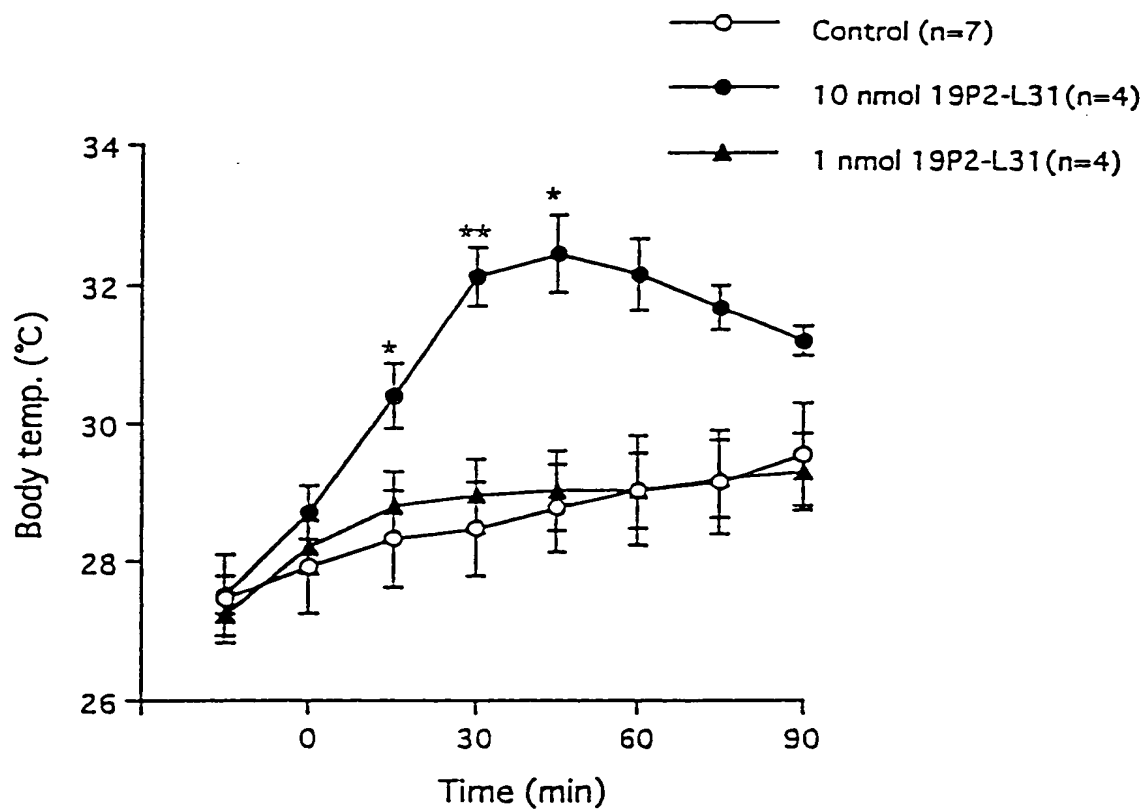


FIG. 45

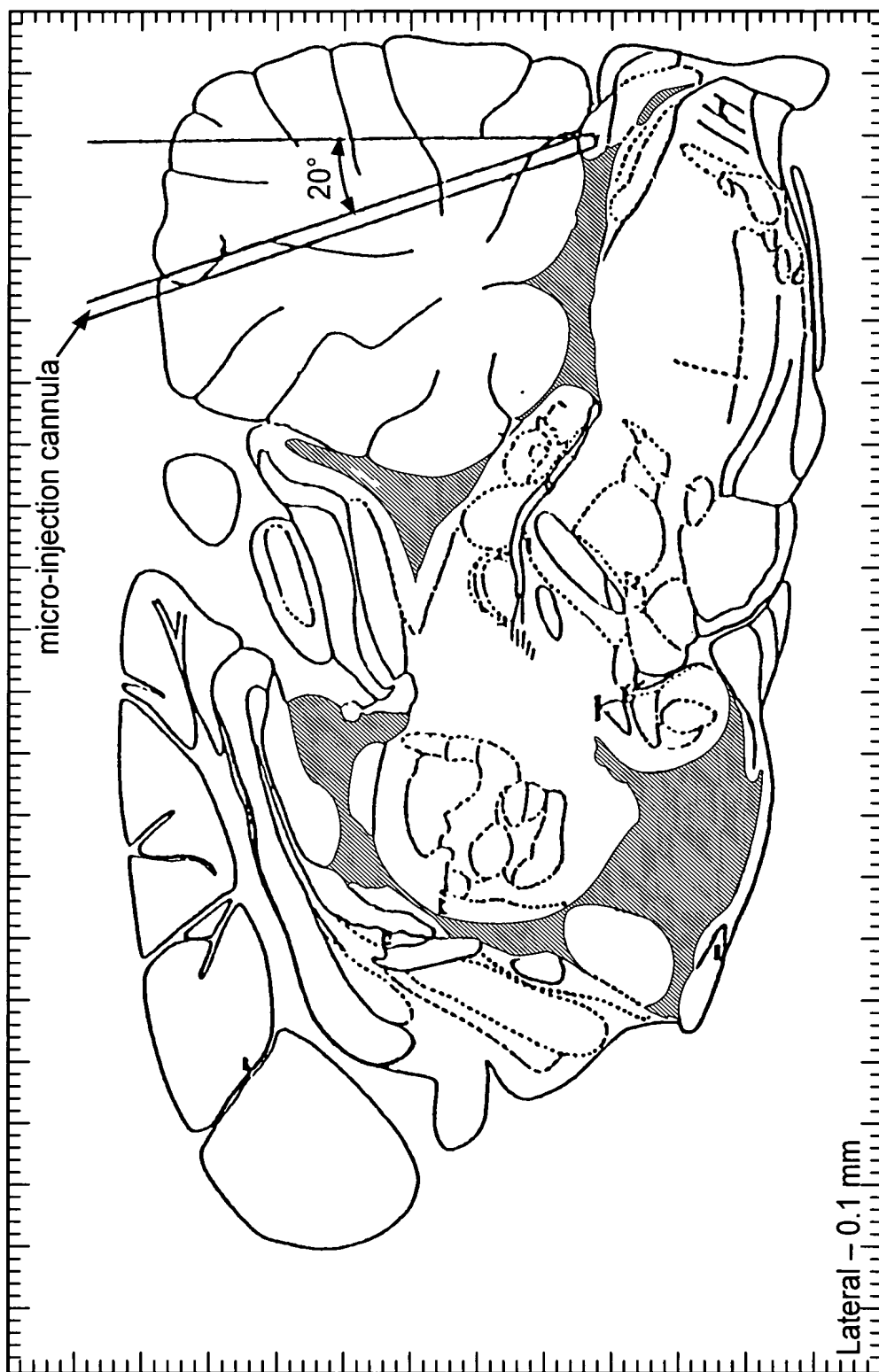


FIG. 46

direct blood pressure

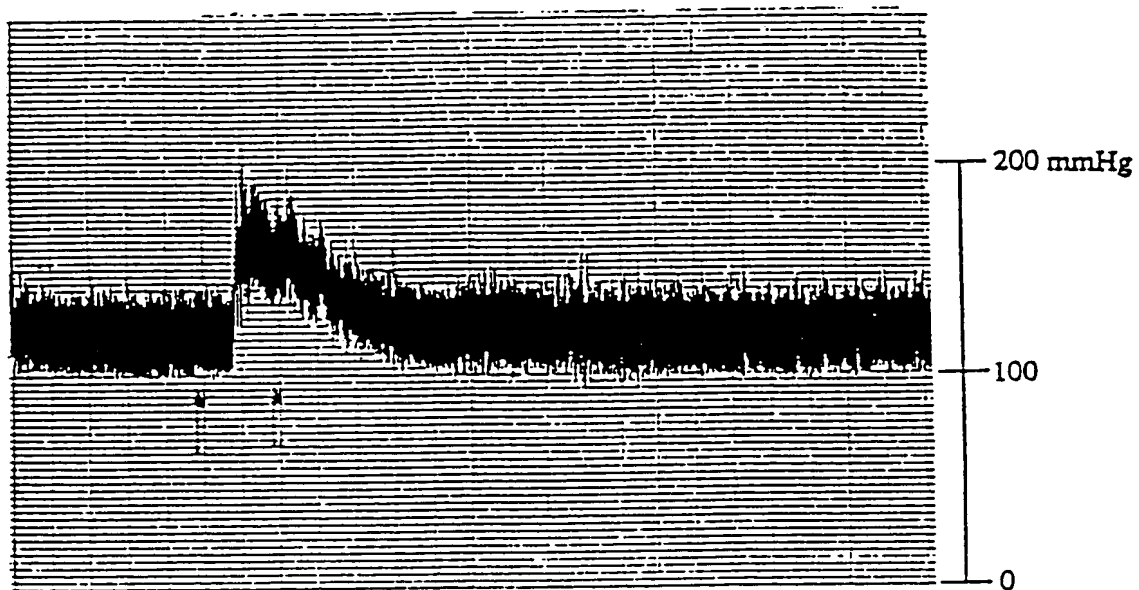


FIG. 47A

mean blood pressure

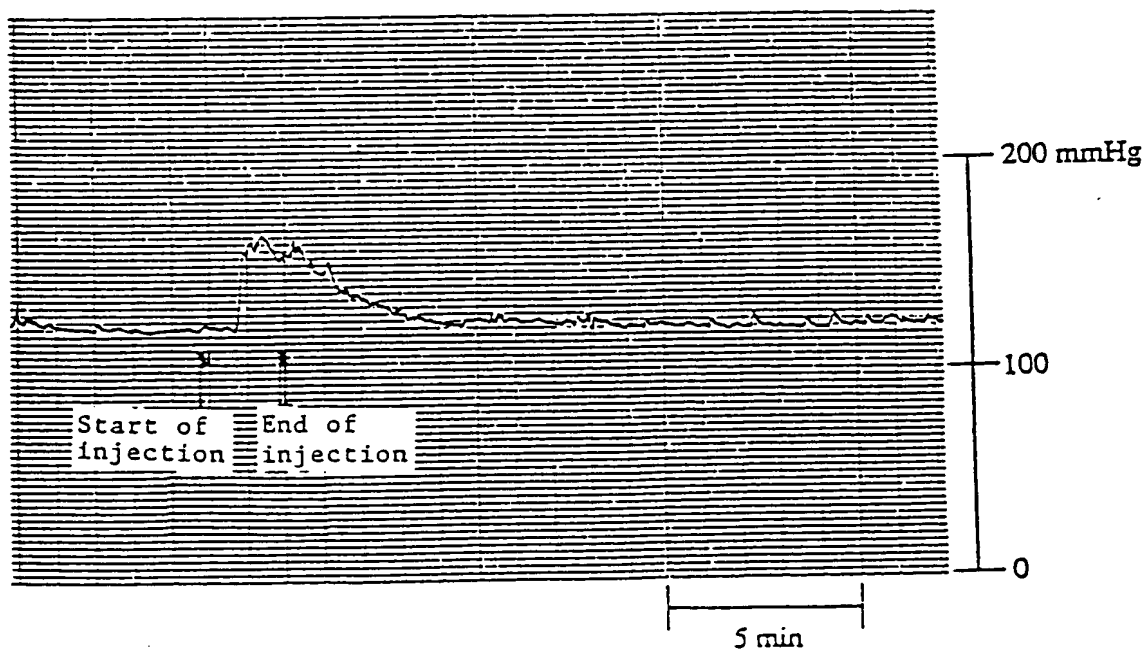


FIG. 47B

53/60

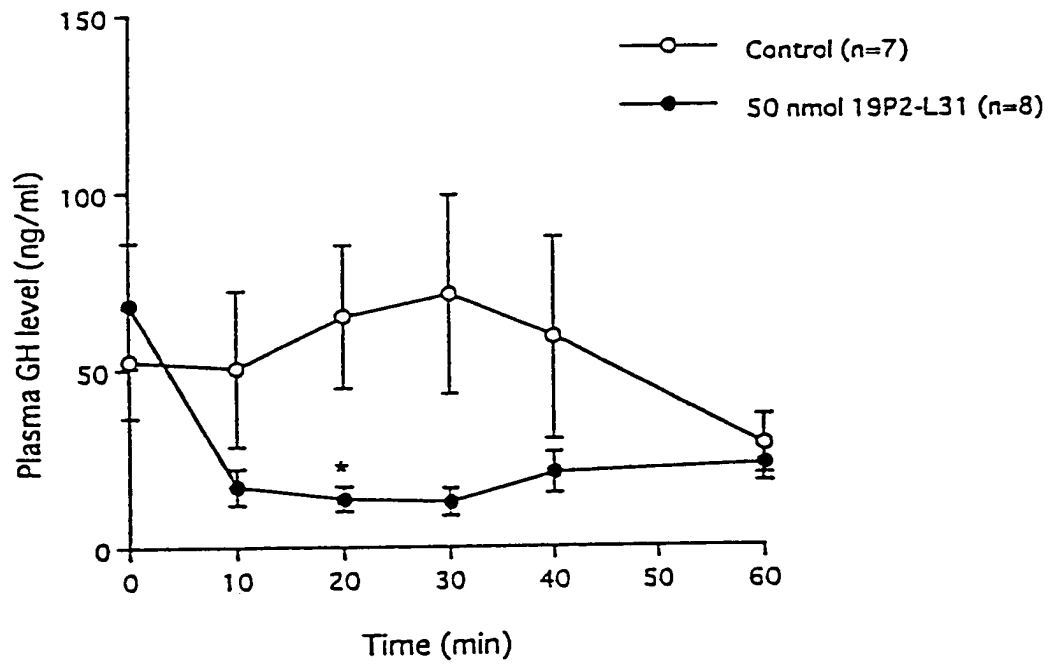


FIG. 48

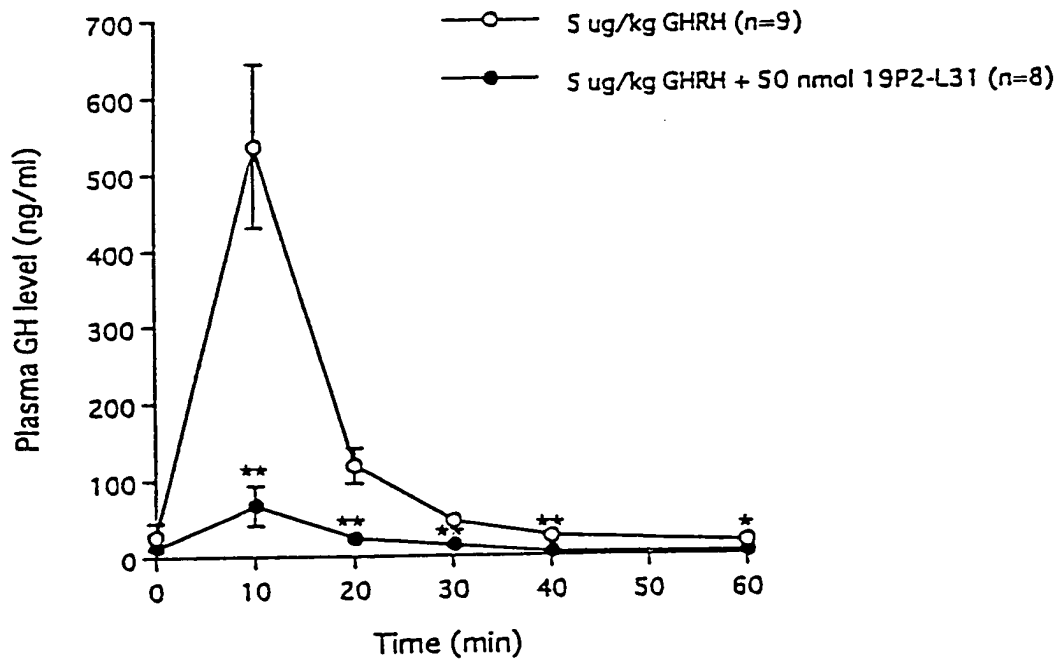


FIG. 49

54/60

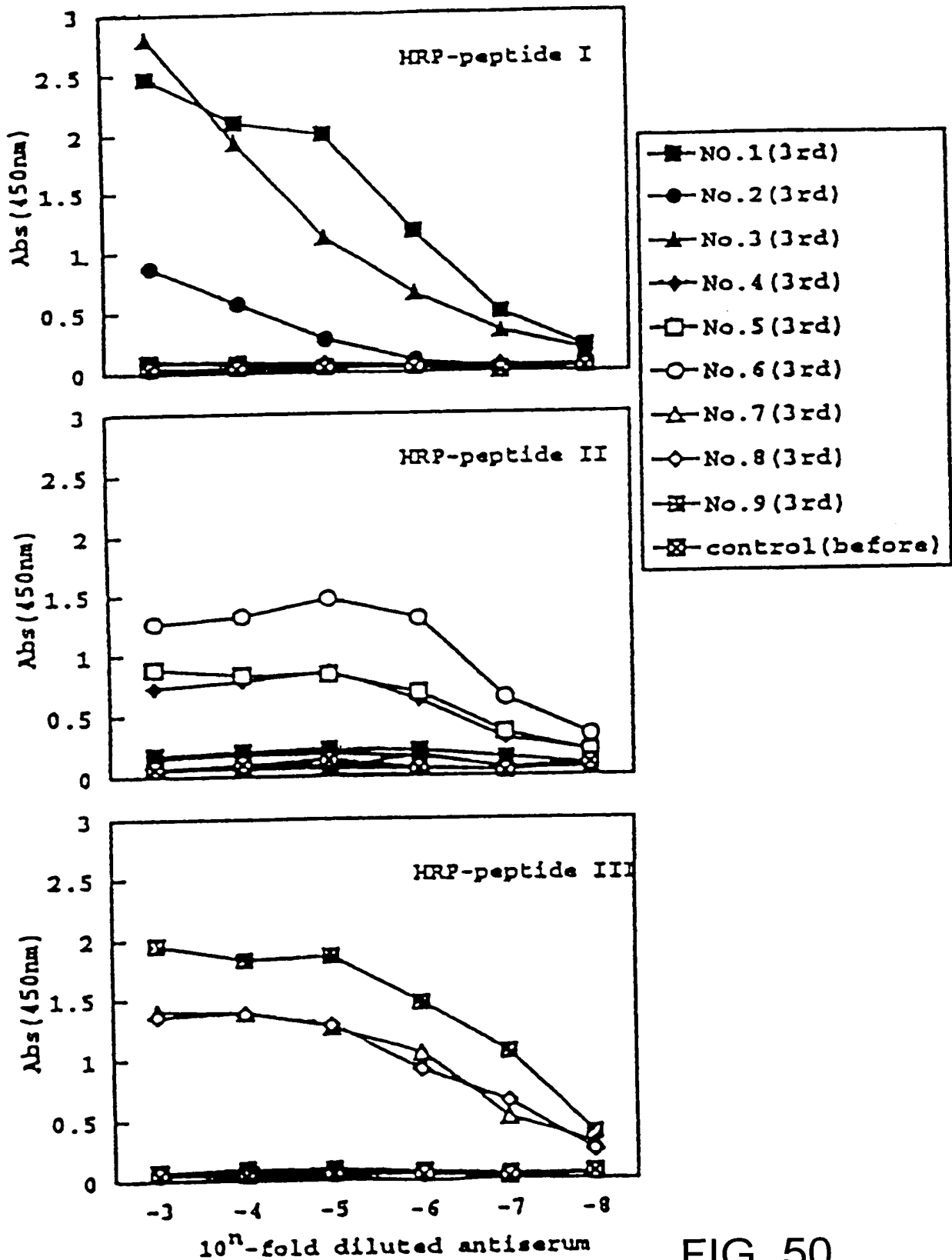


FIG. 50

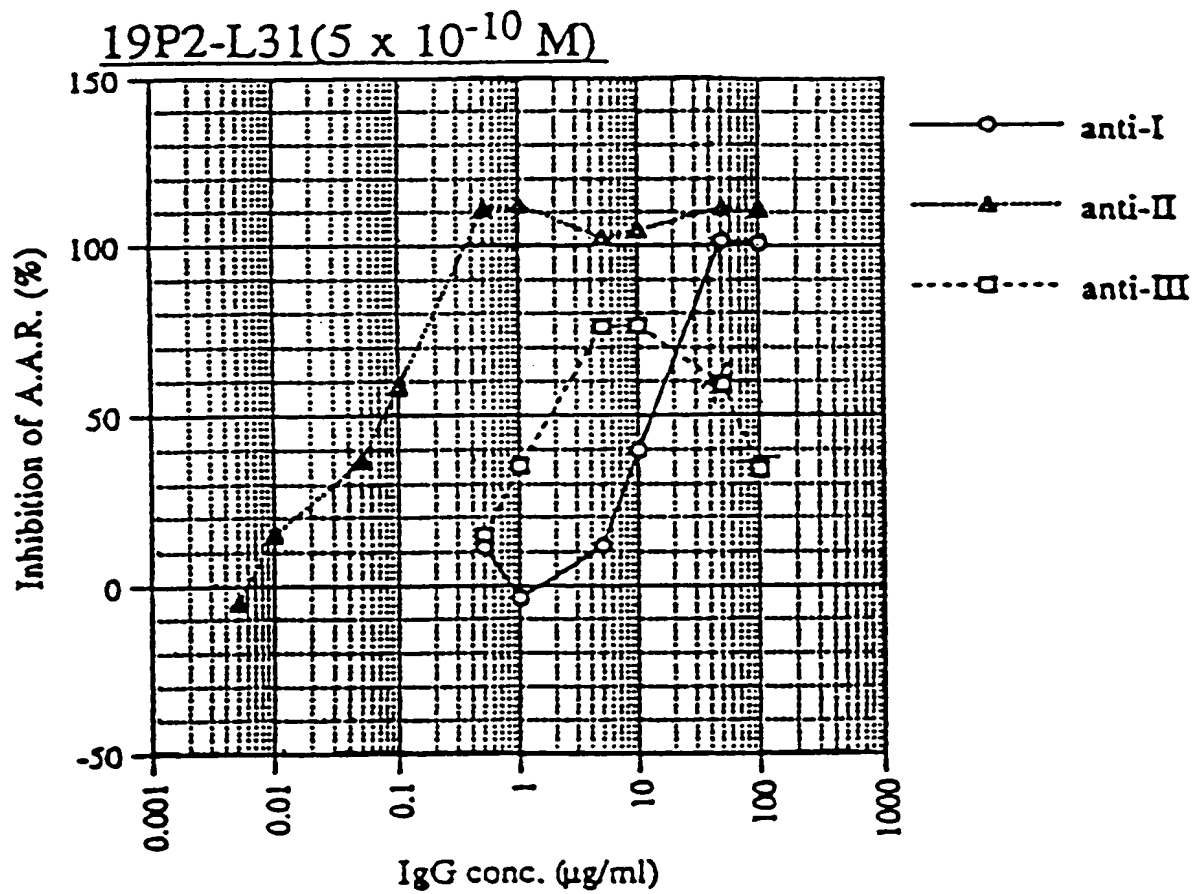


FIG. 51





FIG. 52A
FIG. 52B
FIG. 52C
FIG. 52D
FIG. 52E

FIG. 52A  
FIG. 52

5'	9	18	27	36	45	54
ATG ACC TCA CTG CCC CCT GGA ACC ACT GGG GAC CCC GAT TTG TTT TCT GGG CCG						
---	---	---	---	---	---	---
Met Thr Ser Leu Pro Pro Gly Thr Thr Gly Asp Pro Asp Leu Phe Ser Gly Pro						
63	72	81	90	89	108	
TCG CCA GCC GGC TCC ACT CCA GCC AAC CAG AGT GCA GAG GCT TCA GAG AGC AAT						
---	---	---	---	---	---	---
Ser Pro Ala Gly Ser Thr Pro Ala Asn Gln Ser Ala Glu Ala Ser Glu Ser Asn						



57/60

117	126	135	144	153	162
GTG TCT GCG ACG GTT CCC AGA GCT GCA GCA GTC ACG CCG TTC CAG AGC CTG CAA					
---	---	---	---	---	---
Val Ser Ala Thr Val Pro Arg Ala Ala Val Thr Pro Phe Gln Ser Leu Gln					
171	180	189	198	207	216
CTA GTG CAC CAG CTG AAG GCA GCA CTG ATC GTG ATG CTG TAC AGC ATC GTG GTG GTC					
---	---	---	---	---	---
Leu Val His Gln Leu Lys Ala Leu Ile Val Met Leu Tyr Ser Ile Val Val Val					
225	234	243	252	261	270
GTG GGT CTG GTG GGC AAC TGC CTT CTT GTG CTG CTG ATC GCG CGC GTG CGC CGG					
---	---	---	---	---	---
Val Gly Leu Val Val Gly Asn Cys Leu Leu Val Val Ile Ala Arg Val Arg Arg					
279	288	297	306	315	324
CTG CAC AAC GTG ACC AAC TTC CTC ATC ATC GGC AAC GGC CTG GCC TTC GAT GTG CTC					
---	---	---	---	---	---
Leu His Asn Val Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu					
333	342	351	360	369	378
ATG TGT GCC GCC TGT GTG CCT CTC ACG CTG GCC TAC GCC TTT GAA CCT CGT GGC					
---	---	---	---	---	---
Met Cys Ala Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly					

FIG. 52B

387	396	405	414	423	432
TGG GTG TTC	GGA GGC CTG	TGC CAC CTT	TTC GTT TTC	CAG CTG TTC	CGG GTC ACC
---	---	---	---	---	---
Trp Val Phe	Gly Gly Leu	Cys His Leu	Val Phe Phe	Gln Leu Phe	Pro Val Thr
441	450	459	468	477	486
GTC TAC GTA	TCG GTG TTC	ACA ACC ACA	ATC GCT GTG	GAC CGC TAT	GTT GTG GTT
---	---	---	---	---	---
Val Tyr Val	Ser Val Phe	Thr Thr Thr	Ile Ala Val	Arg Tyr Val	Val Val
495	504	513	522	531	540
CTG GTG CAC	CCG CTA CGT	CGG CGC ATT	TCA CTG AAG	CTC AGC GCC	TAC GCT GTG
---	---	---	---	---	---
Leu Val His	Pro Leu Arg	Arg Arg Ile	Ser Leu Lys	Ser Ala Tyr	Ala Val
549	558	567	576	585	594
CTG GGC ATC	TGG GCT CTA	TCT GCA GTG	CTG GCG CTG	CCG GCC GCG	GTG CAC ACC
---	---	---	---	---	---
Leu Gly Ile	Trp Ala Leu	Ser Ala Val	Leu Ala Leu	Pro Ala Val	His Thr
603	612	621	630	639	648
TAC CAT GTA	GAG CTC AAG	CCC CAC GAC	GTG CGC CTC	TGC GAG GAG	TTC TGG GGT
---	---	---	---	---	---
Tyr His Val	Glu Leu Lys	Pro His Asp	Val Arg Leu	Cys Glu Glu	Phe Trp Gly

FIG. 52C

657	666	675	684	693	702
TCG CAG GAG CGC CAG CGA CAG ATC TAT GCC TGG GGG CTG CTG GGC ACC TAT					
---	---	---	---	---	---
Ser Gln Glu Arg Arg Gln Arg Gln Ile Tyr Ala Trp Gly Leu Leu Gly Thr Tyr					
711	720	729	738	747	756
TTG CTC CCC CTG CTG GGC ATT CTC CTG TCT TAC GTC CGG GTG TCG GTG AAG TTG					
---	---	---	---	---	---
Leu Leu Pro Leu Leu Ala Ile Leu Ser Tyr Val Arg Val Ser Val Lys Leu					
765	774	783	792	801	810
CGG AAC CGC GTG GTG CCT GGC AGC GTG ACC CAG AGC CAG GCT GAC TGG GAC CGA					
---	---	---	---	---	---
Arg Asn Arg Val Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg					
819	828	837	846	855	864
GCG CGT CGC CGT CGC ACT TTC TGC CTG CTG CTG GTG GTG GTG GTG TTC GCG					
---	---	---	---	---	---
Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Ala					
873	882	891	900	909	918
GTC TGC TGG CTG CCT CTG CAC ATT TTC AAC CTG CTG CGG GAC CTG GAC CCG CGT					
---	---	---	---	---	---
Val Cys Trp Leu Pro Leu His Ile Phe Asn Leu Leu Arg Asp Leu Asp Pro Arg					

FIG. 52D



927	GCC ATC GAC CCC TAC GCC	936	TTC GGG CTG GTG CAG CTC	945	954	963	972
---	---	---	---	---	---	---	---
Ala Ile Asp	Pro Tyr Ala Phe Gly Leu Val Gln Leu Cys His Trp Leu Ala						
981	ATG AGC TCC GCC TGC TAC AAC CCC TTC ATC TAT GCG TCG CTG CAC GAC AGC TTC	990	999	1008	1017	1026	
---	---	---	---	---	---	---	---
Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala Ser Leu His Asp Ser Phe							
1035	CGA GAG GAG CTA CGC AAG ATG CTT CTG TCT TGG CCC CGC AAG ATC GTG CCT CAT	1044	1053	1062	1071	1080	
---	---	---	---	---	---	---	---
Arg Glu Glu Leu Arg Lys Met Leu Leu Ser Trp Pro Arg Lys Ile Val Pro His							
1089	GGC CAG AAT ATG ACC GTC AGT GTG GTC ATC TGA TGA	1098	1107	1116			
---	---	---	---	---	---	---	---
Gly Gln Asn Met Thr Val Ser Val Val Ile ---							

FIG. 52E